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PF 15-MAY-1994; 94EP-0303575.
XX
PR 24-MAY-1993; 93US-0068394.
PR 12-AUG-1993; 93US-0106463.
PR 25-AUG-1993; 93US-011758.
PR 03-DEC-1993; 93US-0162407.
PR 07-MAR-1994; 94US-0209502.
PR 11-MAY-1994; 94US-0243345.
XX
XX (IMMUNEX CORP.
XX Beckmann MP, Lyman SD.
XX WPI: 1995-008071/02.
XX N-PSDB: AAG79079.
XX
XX Isolated ligands for flt 3 receptors - useful for treating
XX anaemia, AIDS and various cancers
XX
XX Disclousure: Page 29-30; 33pp; English.
XX
XX A human T-cell lambda-gli0 random primed cDNA library was
XX screened with a fragment corresponding to the extracellular
XX domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAG79076)
XX to isolate human flt3-L cDNA. flt3 stimulates progenitor and
XX stem cells, and can be used e.g. in gene therapy protocols.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 235 AA:
SQ
Query Match 100.0%; Score 1242; DB 16; Length 235;
Best Local Similarity 100.0%; Pred. No. 4.9e-109;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVALPAPMSPTTYLLLLSSGLSTGPCSFQHSPISSDFAVKIRELSDYLLODYPVTV 60
DB 1 MTVALPAPMSPTTYLLLLSSGLSTGPCSFQHSPISSDFAVKIRELSDYLLODYPVTV 60
QY 61 ASNLQDELGCGIMRLVLAORWMERLKTVAAGSKMOGLLEVRNTEIHFTVKCAFOPPPSCL 120
DB 61 ASNLQDELGCGIMRLVLAORWMERLKTVAAGSKMOGLLEVRNTEIHFTVKCAFOPPPSCL 120
QY 121 RFVQNTISRLQETSEDLVALKPMITRONPSRCLQLQCCPDSSSTLPSPSPRLLEATPT 140
DB 121 RFVQNTISRLQETSEDLVALKPMITRONPSRCLQLQCCPDSSSTLPSPSPRLLEATPT 140
QY 181 APQPPILLLLLPVGLLLAAAMCLHWQRTRRTPRPGEGVPPVPSPODLLVEH 235
DB 181 APQPPILLLLLPVGLLLAAAMCLHWQRTRRTPRPGEGVPPVPSPODLLVEH 235
RESULT 2
AAM67769
ID AAM67769 standard; Protein: 235 AA.
XX
XX AAM67769;
XX
XX 25-MAR-1999 (first entry)
XX
XX Human flt3-ligand.
XX
XX Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;
XX immunogenic; autoimmune disease; organ transplantation; food allergy;
XX tissue transplantation.
XX
XX Homo sapiens.
XX
XX OS MO9857655-A1.
XX
XX PD 23-DEC-1998.
XX
XX PF 12-JUN-1998; 98WO-US2085.
XX

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PR 17-JUN-1997; 97US-0857421.
XX
XX (IMMUNEX CORP.
XX Abbott NM, Mowat AM, Viney JL.
XX
XX WPI: 1999-070422/06.
XX
XX N-PSDB: AAV81506.
XX
XX Methods for initiating or enhancing antigen specific immune
XX tolerance - by using murine or human flt3 ligand
XX
XX Claim 1; Page 14-15; 25pp; English.
XX
XX A method has been developed of initiating or enhancing: (i) an antigen-
XX specific immune tolerance; or (ii) immunotolerance of a therapeutic
XX immunogenic molecule by addition of a polypeptide, before, after or with
XX the mucosal administration of an immunotoxin; amount of the antigen
XX or therapeutic molecule, respectively. The polypeptide is capable of
XX binding the flt3 receptor and is: a) amino acids 28-x of murine flt3
XX ligand (flt3-L), where x is an amino acid between 163-231; b) amino
XX acids 28-y of human flt3-L, where y is an amino acid between 160-235;
XX and c) a polypeptide that has at least 90% identity to the polypeptides
XX of either (a) or (b). The method ameliorates the effects of autoimmune
XX diseases, food allergies or organ or tissue rejection following
XX transplantation. Administration of flt3-L allows lower doses of antigens
XX to be used in vivo for mucosally administered antigens. The present
XX sequence represents human flt3-L.
XX
XX Sequence 235 AA:
SQ
Query Match 100.0%; Score 1242; DB 20; Length 235;
Best Local Similarity 100.0%; Pred. No. 4.9e-109;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVALPAPMSPTTYLLLLSSGLSTGPCSFQHSPISSDFAVKIRELSDYLLODYPVTV 60
DB 1 MTVALPAPMSPTTYLLLLSSGLSTGPCSFQHSPISSDFAVKIRELSDYLLODYPVTV 60
QY 61 ASNLQDELGCGIMRLVLAORWMERLKTVAAGSKMOGLLEVRNTEIHFTVKCAFOPPPSCL 120
DB 61 ASNLQDELGCGIMRLVLAORWMERLKTVAAGSKMOGLLEVRNTEIHFTVKCAFOPPPSCL 120
QY 121 RFVQNTISRLQETSEDLVALKPMITRONPSRCLQLQCCPDSSSTLPSPSPRLLEATPT 180
DB 121 RFVQNTISRLQETSEDLVALKPMITRONPSRCLQLQCCPDSSSTLPSPSPRLLEATPT 180
QY 181 APQPPILLLLLPVGLLLAAAMCLHWQRTRRTPRPGEGVPPVPSPODLLVEH 235
DB 181 APQPPILLLLLPVGLLLAAAMCLHWQRTRRTPRPGEGVPPVPSPODLLVEH 235
RESULT 3
AAV69719
ID AAV69719 standard; Protein: 235 AA.
XX
XX AAV69719;
XX
XX 05-JUL-2000 (first entry)
XX
XX Full length wild type human flt-3 protein.
XX
XX Immunomodulator; immunosuppressive; cytostatic; anti-anemic; anti-HIV;
XX neutroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
XX cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
XX cellular expansion; cellular differentiation; natural killer cell;
XX cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
XX myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
XX multiple myeloma; leukemia.
XX
XX Homo sapiens.
XX
XX OS MO200001823-A2.
XX

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XX 13-JAN-2000.
PD 25-JUN-1999; 99WO-US14296.
XX 02-JUL-1998; 98US-0109100.
XX (IMMUNEX CORP.
PA Graddis TJ, McGrew JT;
XX WPI: 2000-182115/16.
DR N-PSDB; AA259064.
XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PI contains amino acid substitutions at positions 8, 84, 118 or 122
XX
PS Claim 1; Page 72-73; 90pp; English.
XX
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (this sequence) or mature (AA69720) flt3-L
CC polypeptides. The flt3-L protein binds cell surface tyrosine kinase
CC receptors and regulate growth and differentiation of hematopoietic
CC progenitor cells. The flt3-L protein can be used to induce cellular
CC expansion (especially in vivo) or differentiation, e.g. in
CC hematopoietic, natural killer (NK) or dendritic cells, especially in the
CC presence of growth factors such as interleukins, colony stimulating
CC factors or protein kinases. The protein can also modulate, augment or
CC enhance a patient's immune response and can be used to treat an immune
CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
CC may be used to treat a pathological condition e.g. myelodysplasia,
CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
CC leukemia.
XX
SQ Sequence 235 AA:
Query Match 100.0%; Score 1242; DB 21; Length 235;
Best Local Similarity 100.0%; Pred. No. 4.9e-109;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVLAPAWSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
DB 1 MTVLAPAWSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
QY 61 ASNODEELCGGLMRLVLAQRMMERLKTVAAGSKMGGILLERNVTEIHFVTKCAFQPPSCL 120
DB 61 ASNODEELCGGLMRLVLAQRMMERLKTVAAGSKMGGILLERNVTEIHFVTKCAFQPPSCL 120
QY 121 REVQTNISRLQETSEQLVAKPMTTRQNFSCRLELCQPPUSSTLPPMSPRPLEVAPT 180
DB 121 REVQTNISRLQETSEQLVAKPMTTRQNFSCRLELCQPPUSSTLPPMSPRPLEVAPT 180
QY 181 AFQPLLLLLLPVGLLLAAACMLHMQRTRRRTPRQEQVPVPSPDOLLIVSH 235
DB 181 AFQPLLLLLLPVGLLLAAACMLHMQRTRRRTPRQEQVPVPSPDOLLIVSH 235

RESULT 4
AAB20192
ID AAB20192 standard; protein; 235 AA.
XX
AC AAB20192;
XX
DT 14-MAY-2001 (first entry)
XX
DF Human Flt-3 ligand.
XX
KW Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
KW immunotherapy; tumour; cancer; melanoma; glioma;
KW lymphoma; autoimmune disease; infection; gene therapy.

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XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..26
XX FT /label= Signal_peptide
XX FT 27..235
XX FT /label= Mature_protein
XX FT Domain 27..182
XX FT /label= Extracellular_domain
XX FT Domain 183..205
XX FT /label= Transmembrane_domain
XX FT Domain 206..235
XX FT /label= Cytoplasmic_domain
XX WO200109303-A2.
XX
XX 08-FEB-2001.
XX
XX 31-JUL-2000; 2000WO-US20679.
XX
XX 30-JUL-1999; 99US-0146170.
XX (VICA-) VICAL INC.
XX
XX Hermanson CG;
XX WPI: 2001-123319/13.
XX N-PSDB; AAF30310.
XX
XX Immunogenic compositions comprising Flt-3 ligand encoding
XX polynucleotide and one or more antigen, or cytokine encoding
XX polynucleotide, useful for suppressing tumour growth and for treating
XX autoimmune diseases (e.g. rheumatoid arthritis).
XX
XX Claim 2; Page 132-133; 149pp; English.
XX
XX The present sequence is that of human fms-like tyrosine kinase
XX (Flt-3 ligand). The invention is directed to enhancing the
XX immune response of a vertebrate to an antigen or a cytokine by
XX administering in vivo, into a tissue of a vertebrate, a Flt-3
XX ligand-encoding polynucleotide, and 1 or more antigen- or
XX cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
XX polynucleotide may encode the present full-length human Flt-3
XX ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185,
XX or 27-235 of the ligand. The polynucleotides are incorporated
XX into the cells of the vertebrate in vivo, and a prophylactically
XX or therapeutically effective amount of flt-3 ligand and 1 or more
XX antigens or cytokines is produced in vivo. Pharmaceuticals;
XX compositions comprising the polynucleotides are useful for
XX suppressing tumour growth in a mammal. The tumour is melanoma,
XX glioma or lymphoma, particularly B-cell lymphoma. They can also
XX be used for the prophylactic and/or therapeutic treatment of:
XX (a) bacterial (e.g. bacillus infections), viral (e.g. hepatitis B
XX and C in humans), parasitic (e.g. malaria) and fungal infections;
XX (b) autoimmune diseases (e.g. rheumatoid arthritis and
XX osteoarthritis); (c) cancer; and (d) Auszsky's disease in pigs.
XX Various other examples of these diseases are given in the
XX specification.
XX
SQ Sequence 235 AA:
Query Match 100.0%; Score 1242; DB 22; Length 235;
Best Local Similarity 100.0%; Pred. No. 4.9e-109;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVLAPAWSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
DB 1 MTVLAPAWSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
QY 61 ASNODEELCGGLMRLVLAQRMMERLKTVAAGSKMGGILLERNVTEIHFVTKCAFQPPSCL 120
DB 61 ASNODEELCGGLMRLVLAQRMMERLKTVAAGSKMGGILLERNVTEIHFVTKCAFQPPSCL 120

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QY 121 RFVQTNISRLQETSEQVLAALKPWITRONFSRCLLEOCOPDSSITLPPWSPRPLEATPT 180
Db 121 RFVQTNISRLQETSEQVLAALKPWITRONFSRCLLEOCOPDSSITLPPWSPRPLEATPT 180

QY 181 APQPLLILLPLVGLLLAAAMCLHMORTRRTRPRGQVPPVPSPODLLLVEH 235
Db 181 APQPLLILLPLVGLLLAAAMCLHMORTRRTRPRGQVPPVPSPODLLLVEH 235

RESULT 5

AA019091 standard; Protein; 235 AA.

AA019091;

22-NOV-2002 (first entry)

C neoformans antigen expressing dendritic cell; related protein #1.

Human; fungicide; fungal infection; dendritic cell; antigen;

Cryptococcus neoformans; vaccine; immunostimulant.

Homo sapiens.

NC020026053-A2.

29-AUG-2002.

14-DEC-2001: 2001MO-US48288.

04-JAN-2001: 2001US-259653P.

(IMMV) IMMUNEX CORP.

Thomas EK;

WPI: 2002-674896/72.

Producing a population of activated, Cryptococcus neoformans

antigen-presenting dendritic cells for preventing or treating C.

neoformans infection comprises causing the obtained dendritic cells to

present the antigen -

Disclosure: Page 25-26; 32pp; English.

The present invention relates to a method of producing a population of

activated, Cryptococcus neoformans antigen-presenting dendritic cells,

comprising causing the obtained dendritic cells to present the antigen

and maturing the dendritic cells. The activated, C. neoformans

antigen-expressing dendritic cells are useful for treating, or as

CC vaccines or vaccine adjuvants against, C. neoformans infection, or for

generating antigen-specific T cells. The present sequence is a human

protein shown in the exemplification of the invention.

Sequence 235 AA:

Query Match 100.0%; Score 1242; DB 23; Length 235;

Best Local Similarity 100.0%; Pred. No. 4.9e-109;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 APQPLLILLPLVGLLLAAAMCLHMORTRRTRPRGQVPPVPSPODLLLVEH 235
Db 181 APQPLLILLPLVGLLLAAAMCLHMORTRRTRPRGQVPPVPSPODLLLVEH 235

RESULT 6

ABG31626
ID ABG31626 standard; Protein; 235 AA.

ABG31626;

29-NOV-2002 (first entry)

Human FLT3L protein.

Tumour; cancer; dendritic cell mobilisation factor; tumour-killing agent;

dendritic cell maturation agent; T cell enhancing factor; skin cancer;

antigen-specific T cell; prostate cancer; liver cancer; bone tumour;

brain tumour; spinal cord tumour; cervical intraepithelial neoplasia;

actinic keratosis; dendritic cell maturation stimulator; cystostatic;

dendritic cell activator; T cell enhancer; human; FLT3L.

Homo sapiens.

NC020026044-A2.

29-AUG-2002.

23-OCT-2001: 2001MO-US46254.

24-OCT-2000: 2000US-242868P.

(IMMV) IMMUNEX CORP.

Thomas EK, Lyman SD, Lynch DH, De Smedt TN, Maliszewski CK;

WPI: 2002-674891/72.

Treating an individual with tumours or cancers, e.g. liver cancer or

brain tumour, by administering a combination of dendritic cell

populations, T cell enhancing factors and activated, antigen-specific T

cells -

Disclosure: Page 38-39; 44pp; English.

The present invention relates to a new method for treating a tumour-

bearing subject. The method involves administering a combination of 2 to

5 agents comprising dendritic cell mobilisation factor, dendritic cell

maturation agent, tumour-killing agent, T cell enhancing factor or

activated, antigen-specific T cells. The method is useful for treating

CC tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver

cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or

cervical intraepithelial neoplasia. The present amino acid sequence

represents the human FLT3L protein that was used in the method of the

invention.

Sequence 235 AA:

Query Match 100.0%; Score 1242; DB 23; Length 235;

Best Local Similarity 100.0%; Pred. No. 4.9e-109;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 AP0PPLLLLLLPVGLLLAAACLMH0RTRRRTRPGE0VPPVSP0DLLVEH 235
 DB 181 AP0PPLLLLLLPVGLLLAAACLMH0RTRRRTRPGE0VPPVSP0DLLVEH 235

RESULT 7

ID ABB08129 standard; protein; 235 AA.

AC ABB08129;

DT 10-SEP-2002 (first entry)

DE Human Flt3L polypeptide.

KM Dendritic cell: mobilisation factor; T cell; adjuvant; antibacterial;
 KM fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;
 KM tuberculosstatic; cytosstatic; human; Flt3L.

OS Homo sapiens.

PN WO200236141-A2.

PD 10-MAY-2002.

PE 30-OCT-2001; 2001WO-US44834.

PR 02-NOV-2000; 2000US-245721P.

PA (IMMUNEX CORP.

PI Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;

PT Thomas EK;

DR WPI; 2002-500114/53.

PT Treating an individual suffering from infection, e.g. inflammation;
 PT chickenpox or AIDS, by administering a combination of dendritic cell
 PT mobilisation factor or maturation agent, T cell enhancing factor and
 PT antigen-specific T cells -

PS Disclosure: Page 37-38; 43pp; English.

CC The invention relates to treating an individual at risk for or suffering
 CC from infection with a pathogenic or opportunistic organism. The method
 CC involves administering a combination of two to five agents comprising:
 CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation
 CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;
 CC or (e) activated, antigen-specific T cells. The methods are useful for
 CC treating an individual at risk for or suffering from infection with a
 CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria
 CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.
 CC T. cruzi, which causes Chaga's disease). The methods are especially
 CC useful for treating an individual suffering from immunosuppression by
 CC enhancing a lymphocyte-mediated immune response. In particular, the
 CC method is useful for treating inflammations, chickenpox, oral or genital
 CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS,
 CC T cell leukemia or T cell lymphoma. The activated antigen-presenting
 CC dendritic cells are useful as a vaccine adjuvant. The present sequence
 CC represents a human Flt3L polypeptide fragment, that can be used as a
 CC dendritic cell mobilisation factor.

SC Sequence 235 AA;

Query Match 100.0%; Score 1242; DB 23; Length 235;

Best Local Similarity 100.0%; Pred. No. 4.9e-109;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLLLSSGSLGSDGSP0HSPISSDPAVKIRELSDYLL0DPYTV 60
 DB 1 MTVALPAMSPPTTYLLLLLLSSGSLGSDGSP0HSPISSDPAVKIRELSDYLL0DPYTV 60

QY 61 ASNI0DEELCGGLMRVLVA0RMERLKTAVGSKM0GLIERVNTIEHFVTKCAF0PPPSCL 120
 DB 61 ASNI0DEELCGGLMRVLVA0RMERLKTAVGSKM0GLIERVNTIEHFVTKCAF0PPPSCL 120
 QY 121 RFV0TINISRL0ETISE0VALKPMITTR0NFSRCL0EQ0QDPSS0TLPPWMSRPLEATPT 180
 DB 121 RFV0TINISRL0ETISE0VALKPMITTR0NFSRCL0EQ0QDPSS0TLPPWMSRPLEATPT 180
 QY 181 AP0PPLLLLLLPVGLLLAAACLMH0RTRRRTRPGE0VPPVSP0DLLVEH 235
 DB 181 AP0PPLLLLLLPVGLLLAAACLMH0RTRRRTRPGE0VPPVSP0DLLVEH 235

RESULT 8

AAG79949

ID AAG79949 standard; protein; 235 AA.

AC AAG79949;

DT 16-MAY-2003 (first entry)

DE Secreted human protein comparison protein #1.

KM Gene: secreted; tyrosine kinase receptor ligand; subfamily:
 KM phosphorylation; kidney; blood; lung; brain glioblastoma; prostate;
 KM color; leukocyte.

OS Unknown.

PN WO2003002138-A1.

PD 09-JAN-2003.

PE 25-JUN-2002; 2002WO-US20172.

PR 27-JUN-2001; 2001US-0891498.

PA (PEKE) PE CORP NY.

PI Gong F, Ceccardi T, Ladunga I;

DR WPI; 2003-267895/26.

PT New isolated human secreted peptide and nucleic acids, useful for the
 PT development of human therapeutics and diagnostic compositions, drug
 PT screening assays, tissue typing and pharmacogenomic analysis -

PS Disclosure: Fig 2A: 66pp; English.

CC The sequences given in AAG79949-50 are included in the scope of the
 CC invention as they show high levels of similarity to the secreted
 CC peptide of the invention. The secreted protein is related to the
 CC lysosine kinase receptor ligand subfamily. This protein effects
 CC protein phosphorylation. The human secreted peptides are useful in
 CC substantial and specific assays related to functional information of
 CC the peptide sequences, to raise antibodies or to elicit immune response,
 CC as reagents in assays that determine the levels of protein in biological
 CC fluids, and as markers for tissues where the corresponding protein is
 CC expressed. The peptides and the antibodies are useful in drug screening
 CC assays, tissue typing and pharmacogenomic analysis. The nucleic acid
 CC molecules are useful as probes, primers and chemical intermediates in
 CC biological assays, for constructing recombinant vectors, and expressing
 CC antigenic portions of the protein. The peptide and nucleic acid
 CC molecules are useful in the identification of therapeutic proteins and
 CC may serve as models or targets for the development of human therapeutic
 CC agents that modulate human secreted peptide activity in cells and
 CC tissues that express the secreted peptide, such as in kidney, blood,
 CC lung, brain glioblastomas, prostate, colon or leukocytes.

SC Sequence 235 AA;

Query Match 100.0%; Score 1242; DB 24; Length 235;

Best Local Similarity 100.0%; Pred. No. 4.9e-109;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLLLSSGLSGTQDCSFQHSPISSSFPAKIRKELSDYLLQDYPVY 60
 DB 1 MTVALPAMSPPTTYLLLLLLSSGLSGTQDCSFQHSPISSSFPAKIRKELSDYLLQDYPVY 60

QY 61 ASNLODEELCGGLRWLYLAQRMERLKTAVGSKMKGILLEVNTIEHFVTKCAFQPPSCL 120
 DB 61 ASNLODEELCGGLRWLYLAQRMERLKTAVGSKMKGILLEVNTIEHFVTKCAFQPPSCL 120

QY 121 REVQTNISRLQETSEOLVALKPWITRONFSRCLELQCPDSSSTLPPEWSPRPLEATAPT 180
 DB 121 REVQTNISRLQETSEOLVALKPWITRONFSRCLELQCPDSSSTLPPEWSPRPLEATAPT 180

QY 181 APOPLLILLLLPVGLLLAAACLMHQRTRRRTPRPGEOVPVPSPQDILLVEH 235
 DB 181 APOPLLILLLLPVGLLLAAACLMHQRTRRRTPRPGEOVPVPSPQDILLVEH 235

RESULT 9
 ABG74239 standard; Protein: 235 AA.

AC ABG74239:
 DT 16-Apr-2003 (first entry)
 DE Human Flt-3 ligand, Flt-3 L.
 KM Human: flt-3 ligand; flt-3 L; stem cell disorder;
 KM cancer: cytopenia; myelodysplastic syndrome; gene therapy
 KM refractory anaemia; chronic myelomonocytic leukaemia;
 KM aplastic anaemia; Fanconi's anaemia; pancythemia; antibody;
 KM bone marrow transplant; cytoreductive therapy; cell expansion;
 KM stem cell mobilisation.
 OS Homo sapiens.
 PN US2002160004-A1.
 PD 31-OCT-2002.
 PF 13-MAR-2002; 2002US-0095449.
 PR 11-MAY-1994; 94US-0243545.
 PR 24-JUN-1996; 96US-0689632.
 PR 24-MAY-1993; 93US-0068394.
 PR 12-AUG-1993; 93US-0106463.
 PR 25-AUG-1993; 93US-0111758.
 PR 03-DEC-1993; 93US-0162407.
 PR 07-MAR-1994; 94US-0209502.
 PR 19-MAY-1995; 95US-0444632.
 PA (LYMA/) LYMAN S D.
 PA (BECK/) BECKMANN M P.
 PI Lyman SD, Beckmann MP;
 DR MPI: 2003-209211/20.
 DR N-PSDB: ABX16545.
 XX New antibody binding mouse flt-3 ligand, useful for screening,
 PT diagnostic and biological assays in disorders with elevated serum
 PT levels of flt-3 ligand, such as Fanconi's and myelodysplastic syndrome,
 PT aplastic and refractory anemia -
 PS Example 4; Page 15-16; 18pp; English.
 CC The invention relates to an antibody that binds to mouse flt-3 ligand
 CC (flt-3 L) encoded by the cDNA insert in vector sfHAV-EG410 in Escherichia
 CC coli DH10B cells having American Type Culture Collection (ATCC)
 CC Accession No. 69286, where the ligand comprises the truncated
 CC extracellular domain of mouse flt-3 L. The methods and compositions are

CC useful for screening, diagnostic and biological assays in disorders
 CC having elevated serum levels of flt-3 ligand, such as cancer, cytopaenia,
 CC myelodysplastic syndromes, stem cell disorders, refractory anaemia,
 CC chronic myelomonocytic leukaemia, aplastic anaemia, Fanconi's anaemia
 CC and pancythemia. Flt-3 L is also useful in allogeneic, syngeneic or
 CC autologous bone marrow transplants in patients undergoing cytoreductive
 CC therapies, as well as cell expansion. Flt-3 L is also useful in gene
 CC therapy and progenitor and stem cell mobilisation systems. The
 CC present sequence represents human flt-3 L.

SQ Sequence 235 AA:
 Query Match 100.0%; Score 1242; DB 24; Length 235;
 Best Local Similarity 100.0%; Pred. No. 4.9e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLLLSSGLSGTQDCSFQHSPISSSFPAKIRKELSDYLLQDYPVY 60
 DB 1 MTVALPAMSPPTTYLLLLLLSSGLSGTQDCSFQHSPISSSFPAKIRKELSDYLLQDYPVY 60

QY 61 ASNLODEELCGGLRWLYLAQRMERLKTAVGSKMKGILLEVNTIEHFVTKCAFQPPSCL 120
 DB 61 ASNLODEELCGGLRWLYLAQRMERLKTAVGSKMKGILLEVNTIEHFVTKCAFQPPSCL 120

QY 121 REVQTNISRLQETSEOLVALKPWITRONFSRCLELQCPDSSSTLPPEWSPRPLEATAPT 180
 DB 121 REVQTNISRLQETSEOLVALKPWITRONFSRCLELQCPDSSSTLPPEWSPRPLEATAPT 180

QY 181 APOPLLILLLLPVGLLLAAACLMHQRTRRRTPRPGEOVPVPSPQDILLVEH 235
 DB 181 APOPLLILLLLPVGLLLAAACLMHQRTRRRTPRPGEOVPVPSPQDILLVEH 235

RESULT 10
 AAG79950 standard; Protein: 235 AA.

AC AAG79950:
 DT 16-MAY-2003 (first entry)
 DE Secreted human protein comparison protein #2.
 KM Gene: secreted; tyrosine kinase receptor ligand; subfamily:
 KM phosphorylation; kidney; blood; lung; brain glioblastoma; prostate;
 KM colon; leukocyte.
 OS Unknown.
 PN WO200302138-A1.
 PD 09-JAN-2003.
 PF 25-JUN-2002; 2002WO-0520172.
 PR 27-JUN-2001; 2001US-0891498.
 PA (PEKE) PE CORP NY.
 PI Gong F, Ceccardi T, Ladunga I;
 DR MPI: 2003-267895/26.
 XX New isolated human secreted peptide and nucleic acids, useful for the
 PT development of human therapeutics and diagnostic compositions, drug
 PT screening assays, tissue typing and pharmacogenomic analysis -
 PS Disclosure; Fig 2B; 66pp; English.
 CC The sequences given in AAG79949-50 are included in the scope of the
 CC invention as they show high levels of similarity to the secreted
 CC peptide of the invention. The secreted protein is related to the
 CC tyrosine kinase receptor ligand subfamily. This protein effects

CC protein phosphorylation. The human secreted peptides are useful in
 CC substantial and specific assays related to functional information of
 CC the peptide sequences, to raise antibodies or to elicit immune response.
 CC as reagents in assays that determine the levels of protein in biological
 CC fluids, and as markers for tissues where the corresponding protein is
 CC expressed. The peptides and the antibodies are useful in drug screening
 CC assays, tissue typing and pharmacogenomic analysis. The nucleic acid
 CC molecules are useful as probes, primers and chemical intermediates in
 CC biological assays, for constructing recombinant vectors, and expressing
 CC antigenic portions of the protein. The peptide and nucleic acid
 CC molecules are useful in the identification of therapeutic proteins and
 CC may serve as models or targets for the development of human therapeutic
 CC agents that modulate human secreted peptide activity in cells and
 CC tissues that express the secreted peptide, such as in kidney, blood,
 CC lung, brain glioblastomas, prostate, colon or leukocytes.

XX Sequence 235 AA:

Query Match 99.6%; Score 1237; DB 24; Length 235;

Best Local Similarity 99.6%; Pred. No. 1.5e-108;

Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVLAPAWSPTTYLLLLLSGLSGTODCSFQHSPISSDFAVKIRLSDYLLQDPYTV 60
 DB 1 MVLAPAWSPTTYLLLLLSGLSGTODCSFQHSPISSDFAVKIRLSDYLLQDPYTV 60
 QY 61 ASNLDDELGGMLRLVLAQRMERLKTAVAGSKMGLLERYNTEIHFTKCAFQPPPSCL 120
 DB 61 ASNLDDELGGMLRLVLAQRMERLKTAVAGSKMGLLERYNTEIHFTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPPMSPRPRLKATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPPMSPRPRLKATAPT 180
 QY 181 APOPLL.LLLLPVGLLLAAACLMHOKTRRRTRPRGEOVPVPSPDILLVEH 235
 DB 181 APOPLL.LLLLPVGLLLAAACLMHOKTRRRTRPRGEOVPVPSPDILLVEH 235

RESULT 11

AAR66175

10 AAR66175 standard; Peptide: 235 AA.

XX AAR66175;

XX 25-MAR-2003 (updated)

DT 10-AUG-1995 (first entry)

XX Human S86/S109 Flt3 ligand peptide sequence.

DE Human S86/S109 Flt3 ligand peptide sequence.

XX Flt3 ligand; tyrosine kinase receptor ligand.

XX Homo sapiens.

XX Homo sapiens.

XX W09426891-A2.

XX 24-NOV-1994.

XX 18-MAY-1994; 94MO-U0505150.

XX 19-MAY-1993; 93US-0065231.

XX 07-JUL-1993; 93US-0089263.

XX 16-JUL-1993; 93US-0092549.

XX 13-AUG-1993; 93US-0106340.

XX 24-AUG-1993; 93US-0112391.

XX 19-NOV-1993; 93US-0155111.

XX 03-DEC-1993; 93US-0162413.

XX (INRA) INST NATI SANTE & RECH MEDICALE.

XX (SCHE) SCHERING CORP.

XX Birnbaum D, Culpepper JA, Hannum CH, Lee FD;

DR WP1: 1995-096787/01.

DR N-PSDB; AAQ79642.

XX New ligand for the Flt3 tyrosine kinase receptor and related

PT nucleic acid, vectors, host cells and antibodies, useful for

PT treating abnormal cell physiology and proliferation, e.g. cancer,

PT also for diagnosis and drug screening

XX Claim 11: Page 76-77; 90pp; English.

CC A cDNA library from the human stromal cell line 293SV40, in
 CC pHEB18, was screened with an 800 bp fragment derived from
 CC mouse clone T112. This fragment encompasses the coding region
 CC conserved between two mouse clones, T118 and T110. Approx. 20
 CC positive clones were selected and partially sequenced. Two
 CC clones, S86 and S109, were found to be approx. 75% homologous
 CC to the mouse clones over the first 163 AAs. Clone S86 continued
 CC to show homology to T110 until the stop codon, although to a
 CC lesser degree, for an overall homology of 66%. Clones T118 and
 CC S109 do not show homology to each other or to the other clones
 CC after mouse residue 163 (human residue 160). An additional mouse
 CC clone designated M88 has a 29 AA insert at the junction between
 CC the common and divergent portions of the mouse ligand.
 CC (updated on 25-MAR-2003 to correct PN field.)

XX Sequence 235 AA:

Query Match 99.5%; Score 1236; DB 16; Length 235;

Best Local Similarity 99.6%; Pred. No. 1.8e-108;

Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVLAPAWSPTTYLLLLLSGLSGTODCSFQHSPISSDFAVKIRLSDYLLQDPYTV 60
 DB 1 MVLAPAWSPTTYLLLLLSGLSGTODCSFQHSPISSDFAVKIRLSDYLLQDPYTV 60
 QY 61 ASNLDDELGGMLRLVLAQRMERLKTAVAGSKMGLLERYNTEIHFTKCAFQPPPSCL 120
 DB 61 ASNLDDELGGMLRLVLAQRMERLKTAVAGSKMGLLERYNTEIHFTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPPMSPRPRLKATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPPMSPRPRLKATAPT 180
 QY 181 APOPLL.LLLLPVGLLLAAACLMHOKTRRRTRPRGEOVPVPSPDILLVEH 235
 DB 181 APOPLL.LLLLPVGLLLAAACLMHOKTRRRTRPRGEOVPVPSPDILLVEH 235

RESULT 12

AAR20194

10 AAR20194 standard; Protein: 235 AA.

XX AAR20194;

XX 14-MAY-2001 (first entry)

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;

XX immunotherapy; therapy; tumour; cancer; melanoma; glioma;

XX lymphoma; autoimmune disease; infection; gene therapy.

XX Homo sapiens.

XX Homo sapiens.

XX Key

XX Peptide

XX Protein

XX Domain

XX Domain

XX Domain

Location/Qualifiers

1..26

/label= signal_peptide

27..235

/label= mature_protein

27..182

/label= Extracellular_domain

183..205

/label= Transmembrane_domain


```

Db      122 ITRNFSCLCLOCPDPSSTLPWPSPRPPLAATAAPQPPDLLLLPVGLLLAAAWC 182
QY      205 LHMOTRRRRTRPPGEQVPPVPSDILLVH 235
      182 LHMOTRRRRTRPPGEQVPPVPSDILLVH 212

RESULT 14
AA69007
ID      AAW69007 standard; poplite; 209 AA.
XX
AC      AAW69007;
XX
DT      01-OCT-1998 (first entry)
XX
DE      Human flt-3 receptor agonist.
XX
KM      Human; flt-3 receptor agonist; haematopoietic cell stimulation; cancer;
KM      bone marrow reconstitution; haematological disease; immune deficiency;
KM      drug-induced myelosuppression; renal dialysis; gene therapy; infection;
KM      congenital metabolic disease; neurological disease; therapy;
KM      dendritic cell production.
XX
OS      Homo sapiens.
XX
PN      MO9818923-A1.
XX
PD      07-MAY-1998.
XX
PE      23-OCT-1997; 97MO-US18700.
XX
PR      25-OCT-1996; 96US-0030094.
XX
PA      (SEAR ) SEARLE & CO G D.
XX
PI      Feng Y, McKeern JP, McWhorter CA, Minnerly JC, Munster NI;
PI      Staten NR, Streeter PR, Moulte SL;
DR      WPI: 1998-272218/24.
XX
PT      Rearranged flt-3 receptor agonists and nucleic acids encoding them -
PT      used to stimulate production of haematopoietic and dendritic cells,
PT      for treatment of haematological diseases, bone marrow reconstitution
PT      and in gene therapy
XX
PS      Disclosure: Page 9-10; 158pp; English.
XX
CC      This sequence represents a rearranged human flt-3 receptor agonists or
CC      the invention. The agonists have a modified flt-3 ligand amino acid
CC      sequence. The agonists are used to stimulate production of haematopoietic
CC      cells in vivo (e.g. in a subject about to donate blood) or for ex vivo
CC      expansion for subsequent transplantation, e.g. to reconstitute bone
CC      marrow after chemotherapy, disease etc., or to treat haematological
CC      disease such as drug-induced myelosuppression, defects caused by
CC      infections, burns or renal dialysis. Optionally ex vivo expanded cells
CC      are transduced with a gene therapy vector for treating e.g. congenital
CC      metabolic diseases, immune deficiency, neurological disease, cancer and
CC      infections. The agonists can also be used in the treatment of tumours,
CC      infections and autoimmune disease. When administered optionally with an
CC      antigen. The agonist can also be used in the production of dendritic
CC      cells for use as an immunising adjuvant for treatment disorders including
CC      acquired immune deficiency syndrome. Compared with native ligands, the
CC      agonists have better stimulatory activity, reduced side effects
CC      and/or better physical properties such as solubility, stability or refold
CC      efficiency. When used together with other stimulatory agents, the
CC      agonists provide a synergistic effect.
XX
SU      Sequence 209 AA:
XX
Query Match      89.7%; Score 114; DB 19; Length 209;
Host Local Similarity 100.0%; Pred. No 5; Le-97;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      27 TQCSFQHSPTISSQFAVKIRELSIDYLLQDYVVTASNDQDELCGGLMRLVLAQRMERL 86
      1 TQDCSFQHSPTISSQFAVKIRELSIDYLLQDYVVTASNDQDELCGGLMRLVLAQRMERL 60
QY      87 KTVASGSKMOGLIERVNTLHFVTKCAFPQPPSCIRFVQNTNSRLLOESTBOLVTKMWT 146
      61 KTVASGSKMOGLIERVNTLHFVTKCAFPQPPSCIRFVQNTNSRLLOESTBOLVTKMWT 120
Db      121 RQNFSCRLCLOCPDPSSTLPWPSPRPPLAATAAPQPPDLLLLPVGLLLAAACLN 180
QY      207 WQTRRRTRPPGEQVPPVPSDILLVH 235
      181 WQTRRRTRPPGEQVPPVPSDILLVH 209

RESULT 15
AA69720
ID      AAY69720 standard; Protein; 209 AA.
XX
AC      AAY69720;
XX
CT      05-JUL-2000 (first entry)
XX
DE      Mature wild type human flt-3 protein.
XX
KM      Immunomodulator; immunosuppressive; cytostatic; anti-tumour; anti-HIV;
KM      neutroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
KM      cell surface tyrosine kinase receptor; haematopoietic progenitor cell;
KM      cellular expansion; cellular differentiation; natural killer cell;
KM      cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KM      myeloid dysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KM      multiple myeloma; leukemia.
XX
OS      Homo sapiens.
XX
PN      MO200001823-A2.
XX
PD      13-JAN-2000.
XX
PE      25-JUN-1999; 99MO-US14296.
XX
PR      02-JUL-1998; 98US-0109100.
XX
PA      (IMMV ) IMMUNEX CORP.
XX
PI      Graddis TJ, McGrew JT;
XX
DR      WPI: 2000-18215/16.
XX
PT      N-PSDB: AAZ59064.
XX
CC      Mutant soluble flt3 ligand polypeptide used in cellular expansion,
CC      immune response stimulation or treatment of pathological conditions
CC      contains amino acid substitutions at positions 8, 84, 118 or 122
XX
PS      Claim 1. Page 89-90; 90pp; English.
XX
CC      The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC      which exhibits increased or decreased biological activity relative to
CC      the full length wild type (AAY69719) or mature (this sequence) flt3-L
CC      polypeptides. The flt3-L protein binds cell surface tyrosine kinase
CC      receptors and regulate growth and differentiation of haematopoietic
CC      progenitor cells. The flt3-L protein can be used to induce cellular
CC      expansion (especially in vivo) or differentiation, e.g. in
CC      haematopoietic, natural killer (NK) or dendritic cells, especially in the
CC      presence of growth factors such as interleukins, colony stimulating
CC      factors or protein kinases. The protein can also modulate, augment or
CC      enhance a patient's immune response and can be used to treat an immune
CC      disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
CC      may be used to treat a pathological condition e.g. myelodysplasia,
CC      aplastic anemia, HIV infection, breast, small cell lung, testicular or
CC      ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute

```

CC leukemia.

XX
SQ Sequence 209 AA;Query Match 89.7%; Score 1114; DB 21; Length 209;
Best Local Similarity 100.0%; Pred. No. 5,1e-97;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 27 | TODCSFOHSPISSDFAVKIRELSDYLDQYPTVASNIQDEELCGGLMRLYLAQRMRERL | 86 |
| Db | 1 | TODCSFOHSPISSDFAVKIRELSDYLDQYPTVASNIQDEELCGGLMRLYLAQRMRERL | 60 |
| QY | 87 | KTVAGSKMGLERVNTIEHFVTKCAFQPPSCIRFVQTNISRLIOETSEOLVALKPMIT | 146 |
| Db | 61 | KTVAGSKMGLERVNTIEHFVTKCAFQPPSCIRFVQTNISRLIOETSEOLVALKPMIT | 120 |
| QY | 147 | RQNFSCLELQCPDSSSTLPPWSPRPLEATAPAPPPLLLL.LPVGLLLAAACLI | 206 |
| Db | 121 | RQNFSCLELQCPDSSSTLPPWSPRPLEATAPAPPPLLLL.LPVGLLLAAACLI | 180 |
| QY | 207 | WQTRRRTRPGEQVPPVPSPODLLVEH | 235 |
| Db | 181 | WQTRRRTRPGEQVPPVPSPODLLVEH | 203 |

Search completed: September 15, 2003, 15:54:23
Job time : 61.515 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: September 15, 2003, 15:52:22 : Search time 20.676 Seconds
(without alignments)
480.899 Million cell updates/sec

Title: US-09-448-378-1
Perfect score: 1242
Sequence: 1 MVLAPAWSPRTYLLLL.....PGEQVVPVSPDLLVEH 235

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/prodata/1/iaa/5A-COMB.pep:*
3: /cgn2_6/prodata/1/iaa/5B-COMB.pep:*
4: /cgn2_6/prodata/1/iaa/5A-COMB.pep:*
5: /cgn2_6/prodata/1/iaa/5B-COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfillsi.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------------------------|
| 1 | 1242 | 100.0 | 235 | 1 | US-08-243-545-6 Sequence 6, Appl. |
| 2 | 1242 | 100.0 | 235 | 2 | US-08-993-962-6 Sequence 6, Appl. |
| 3 | 1242 | 100.0 | 235 | 3 | US-09-160-841-6 Sequence 6, Appl. |
| 4 | 1242 | 100.0 | 235 | 3 | US-09-109-100-1 Sequence 6, Appl. |
| 5 | 1242 | 100.0 | 235 | 5 | PCT-US94-05365-5 Sequence 6, Appl. |
| 6 | 1124 | 90.5 | 212 | 3 | US-09-109-100-10 Sequence 18, Appl. |
| 7 | 1114 | 89.7 | 209 | 3 | US-09-109-100-18 Sequence 10, Appl. |
| 8 | 1110 | 89.4 | 209 | 3 | US-09-109-100-9 Sequence 9, Appl. |
| 9 | 1110 | 89.4 | 209 | 3 | US-09-109-100-12 Sequence 12, Appl. |
| 10 | 1110 | 89.4 | 209 | 3 | US-09-109-100-14 Sequence 14, Appl. |
| 11 | 1110 | 89.4 | 209 | 3 | US-09-109-100-11 Sequence 17, Appl. |
| 12 | 1108 | 89.2 | 209 | 3 | US-09-109-100-11 Sequence 11, Appl. |
| 13 | 1108 | 89.1 | 209 | 3 | US-09-109-100-15 Sequence 15, Appl. |
| 14 | 1107 | 89.1 | 209 | 3 | US-09-109-100-13 Sequence 13, Appl. |
| 15 | 1106 | 89.0 | 209 | 3 | US-09-109-100-8 Sequence 8, Appl. |
| 16 | 1100 | 88.6 | 209 | 3 | US-09-109-100-16 Sequence 16, Appl. |
| 17 | 895.5 | 72.1 | 234 | 4 | US-09-322-409-7 Sequence 7, Appl. |
| 18 | 895.5 | 72.1 | 234 | 4 | US-09-451-527-7 Sequence 7, Appl. |
| 19 | 894.5 | 72.0 | 231 | 4 | US-09-322-409-44 Sequence 44, Appl. |
| 20 | 894.5 | 72.0 | 231 | 4 | US-09-451-527-44 Sequence 44, Appl. |
| 21 | 797.5 | 64.2 | 268 | 4 | US-09-322-409-23 Sequence 23, Appl. |
| 22 | 797.5 | 64.2 | 268 | 4 | US-09-451-527-23 Sequence 23, Appl. |
| 23 | 796.5 | 64.1 | 276 | 4 | US-09-322-409-26 Sequence 26, Appl. |
| 24 | 796.5 | 64.1 | 276 | 4 | US-09-451-527-26 Sequence 26, Appl. |
| 25 | 791.5 | 63.7 | 265 | 4 | US-09-322-409-49 Sequence 49, Appl. |
| 26 | 791.5 | 63.7 | 265 | 4 | US-09-451-527-49 Sequence 49, Appl. |
| 27 | 768.5 | 61.9 | 231 | 1 | US-08-243-545-2 Sequence 2, Appl. |

| | | | | | | |
|----|-------|------|-----|---|-------------------|--------------------|
| 28 | 768.5 | 61.9 | 231 | 2 | US-08-993-962-2 | Sequence 2, Appl. |
| 29 | 768.5 | 61.9 | 231 | 3 | US-09-160-841-2 | Sequence 2, Appl. |
| 30 | 768.5 | 61.9 | 231 | 5 | PCT-US94-05365-2 | Sequence 2, Appl. |
| 31 | 765.5 | 61.6 | 231 | 1 | US-08-220-3798-7 | Sequence 7, Appl. |
| 32 | 765.5 | 61.6 | 231 | 5 | PCT-US95-03866-6 | Sequence 6, Appl. |
| 33 | 698.5 | 56.2 | 250 | 4 | US-09-322-409-31 | Sequence 31, Appl. |
| 34 | 698.5 | 56.2 | 250 | 4 | US-09-451-527-31 | Sequence 31, Appl. |
| 35 | 506.5 | 40.8 | 137 | 3 | US-09-109-100-19 | Sequence 19, Appl. |
| 36 | 154 | 12.4 | 42 | 5 | PCT-US94-05150-17 | Sequence 17, Appl. |
| 37 | 91.5 | 7.4 | 675 | 1 | US-08-317-522A-9 | Sequence 9, Appl. |
| 38 | 91.5 | 7.4 | 675 | 1 | US-08-439-8-8A-9 | Sequence 9, Appl. |
| 39 | 91.5 | 7.4 | 675 | 2 | US-08-751-965-9 | Sequence 9, Appl. |
| 40 | 91.5 | 7.4 | 675 | 2 | US-08-738-975-9 | Sequence 9, Appl. |
| 41 | 91.5 | 7.4 | 675 | 2 | US-08-728-626-9 | Sequence 9, Appl. |
| 42 | 91.5 | 7.4 | 675 | 3 | US-08-808-559A-9 | Sequence 9, Appl. |
| 43 | 89.5 | 7.2 | 941 | 4 | US-09-390-134B-31 | Sequence 31, Appl. |
| 44 | 87.5 | 7.0 | 415 | 3 | US-09-006-353A-6 | Sequence 6, Appl. |
| 45 | 87.5 | 7.0 | 415 | 4 | US-09-573-966-6 | Sequence 6, Appl. |

ALIGNMENTS

RESULT :
US-08-243-545-6
Sequence 6, Application US/08243545
Patent No. 5594512
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flk3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
Z-IP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids

TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-243-545-6

Query Match 100.0%: Score 1242; DB 1: Length 235;
 Best Local Similarity 100.0%; Pred. No. 2, 3e-117;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQSPSSDFAVKIRLSYLLQGYEVTV 60
 DB 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQSPSSDFAVKIRLSYLLQGYEVTV 60
 QY 61 ASNLODEELCGGLVLAQRMERLKTVAASKMOGLLEEVNTLEIHFVTKCAFQPPPSCL 120
 DB 61 ASNLODEELCGGLVLAQRMERLKTVAASKMOGLLEEVNTLEIHFVTKCAFQPPPSCL 120
 QY 121 RRVQTNISRLQETSEQLVALKPMTTRQNSRCLELCCQPPSSSTLPPWSPRPLEATAPT 180
 DB 121 RRVQTNISRLQETSEQLVALKPMTTRQNSRCLELCCQPPSSSTLPPWSPRPLEATAPT 180
 QY 181 AQPPLLLLLLPVGLLLAAAWCLHMQRTRPRRPRGEOVPPVPSQDILLVEH 235
 DB 181 AQPPLLLLLLPVGLLLAAAWCLHMQRTRPRRPRGEOVPPVPSQDILLVEH 235

RESULT 2
 US-08-993-962-6
 Sequence 6, Application US/08993962
 Patent No. 5843423

GENERAL INFORMATION:
 APPLICANT: Lyman, Stewart D.
 APPLICANT: Beckmann, M. Patricia
 TITLE OF INVENTION: Ligands for fli3/fik-2 Receptors
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Stephen L. Malaska, Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.0.1
 SOFTWARE: Microsoft Word, Version #5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/993,962
 FILING DATE: December 18, 1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/162,407
 FILING DATE: December 3, 1993
 APPLICATION NUMBER: 08/111,758
 FILING DATE: August 25, 1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/106,463
 FILING DATE: August 12, 1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/068,394
 FILING DATE: May 24, 1993
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Malaska, Stephen L.
 REGISTRATION NUMBER: 32,655
 REFERENCE/DOCKET NUMBER: 2813-C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 235 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-993-962-6

Query Match 100.0%: Score 1242; DB 2: Length 235;
 Best Local Similarity 100.0%; Pred. No. 2, 3e-117;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQSPSSDFAVKIRLSYLLQGYEVTV 60
 DB 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQSPSSDFAVKIRLSYLLQGYEVTV 60
 QY 61 ASNLODEELCGGLVLAQRMERLKTVAASKMOGLLEEVNTLEIHFVTKCAFQPPPSCL 120
 DB 61 ASNLODEELCGGLVLAQRMERLKTVAASKMOGLLEEVNTLEIHFVTKCAFQPPPSCL 120
 QY 121 RRVQTNISRLQETSEQLVALKPMTTRQNSRCLELCCQPPSSSTLPPWSPRPLEATAPT 180
 DB 121 RRVQTNISRLQETSEQLVALKPMTTRQNSRCLELCCQPPSSSTLPPWSPRPLEATAPT 180
 QY 181 AQPPLLLLLLPVGLLLAAAWCLHMQRTRPRRPRGEOVPPVPSQDILLVEH 235
 DB 181 AQPPLLLLLLPVGLLLAAAWCLHMQRTRPRRPRGEOVPPVPSQDILLVEH 235

RESULT 3
 US-09-160-841-5
 Sequence 6, Application US/09160841
 Patent No. 6190655

GENERAL INFORMATION:
 APPLICANT: Lyman, Stewart D.
 APPLICANT: Beckmann, M. Patricia
 TITLE OF INVENTION: Ligands for fli3/fik-2 Receptors
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Stephen L. Malaska, Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.0.1
 SOFTWARE: Microsoft Word, Version #5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/160,841
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/162,407
 FILING DATE: December 3, 1993
 APPLICATION NUMBER: 08/111,758
 FILING DATE: August 25, 1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/106,463
 FILING DATE: August 12, 1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/068,394
 FILING DATE: May 24, 1993
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Malaska, Stephen L.
 REGISTRATION NUMBER: 32,655
 REFERENCE/DOCKET NUMBER: 2813-C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2003, 15:57:23 ; Search time 40.3433 Seconds
(without alignments)
849.940 Million cell updates/sec

Title: US-09-448-378-1
Perfect score: 1242
Sequence: 1 MTVLADAMSPRTYLLLL.....RPGEQVPVPSPQDLLVERH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description: |
|------------|-------|-------------|--------|-------|------------------|
| 1 | 1242 | 100.0 | 235 | 7 | US-08-994-468-6 |
| 2 | 1242 | 100.0 | 235 | 9 | US-09-448-378-1 |
| 3 | 1242 | 100.0 | 235 | 10 | US-09-983-806-6 |
| 4 | 1242 | 100.0 | 235 | 10 | US-09-904-536-1 |
| 5 | 1242 | 100.0 | 235 | 12 | US-10-314-035-6 |
| 6 | 1242 | 100.0 | 235 | 14 | US-10-095-449-6 |
| 7 | 1242 | 100.0 | 235 | 15 | US-10-241-927-2 |
| 8 | 1124 | 90.5 | 212 | 10 | US-09-904-536-10 |
| 9 | 1114 | 89.7 | 209 | 10 | US-09-904-536-18 |
| 10 | 1110 | 89.4 | 209 | 10 | US-09-904-536-9 |
| 11 | 1110 | 89.4 | 209 | 10 | US-09-904-536-12 |
| 12 | 1110 | 89.4 | 209 | 10 | US-09-904-536-14 |
| 13 | 1110 | 89.4 | 209 | 10 | US-09-904-536-17 |
| 14 | 1108 | 89.2 | 209 | 10 | US-09-904-536-11 |
| 15 | 1108 | 89.2 | 209 | 10 | US-09-904-536-15 |

| 16 | 1107 | 89.1 | 209 | 10 | US-09-904-536-13 | Sequence 13, Appl |
|----|-------|------|-----|----|--------------------|-------------------|
| 17 | 1106 | 89.0 | 209 | 10 | US-09-904-536-8 | Sequence 16, Appl |
| 18 | 1100 | 88.6 | 209 | 10 | US-09-904-536-16 | Sequence 8, Appl |
| 19 | 895.5 | 72.1 | 294 | 12 | US-10-262-439-7 | Sequence 7, Appl |
| 20 | 895.5 | 72.0 | 294 | 15 | US-10-218-654-7 | Sequence 7, Appl |
| 21 | 894.5 | 72.0 | 291 | 12 | US-10-262-439-44 | Sequence 44, Appl |
| 22 | 894.5 | 72.0 | 291 | 15 | US-10-218-654-44 | Sequence 44, Appl |
| 23 | 882 | 66.2 | 356 | 15 | US-10-051-355A-1 | Sequence 1, Appl |
| 24 | 797.5 | 64.2 | 268 | 12 | US-10-262-439-23 | Sequence 23, Appl |
| 25 | 797.5 | 64.1 | 276 | 12 | US-10-218-654-23 | Sequence 23, Appl |
| 26 | 796.5 | 64.1 | 276 | 15 | US-10-262-439-26 | Sequence 26, Appl |
| 27 | 796.5 | 64.1 | 276 | 15 | US-10-218-654-26 | Sequence 26, Appl |
| 28 | 791.5 | 63.7 | 265 | 12 | US-10-262-439-49 | Sequence 49, Appl |
| 29 | 791.5 | 63.7 | 265 | 15 | US-10-218-654-49 | Sequence 49, Appl |
| 30 | 768.5 | 61.9 | 231 | 7 | US-08-994-468-2 | Sequence 2, Appl |
| 31 | 768.5 | 61.9 | 231 | 9 | US-09-448-378-2 | Sequence 2, Appl |
| 32 | 768.5 | 61.9 | 231 | 10 | US-09-563-806-2 | Sequence 2, Appl |
| 33 | 768.5 | 61.9 | 231 | 12 | US-10-314-035-2 | Sequence 2, Appl |
| 34 | 768.5 | 61.9 | 231 | 14 | US-10-095-449-2 | Sequence 2, Appl |
| 35 | 698.5 | 56.2 | 250 | 12 | US-10-262-439-31 | Sequence 31, Appl |
| 36 | 698.5 | 56.2 | 250 | 15 | US-10-218-654-31 | Sequence 31, Appl |
| 37 | 506.5 | 40.8 | 137 | 10 | US-09-904-536-19 | Sequence 19, Appl |
| 38 | 97.5 | 7.9 | 658 | 12 | US-10-304-946-14 | Sequence 14, Appl |
| 39 | 91.5 | 7.4 | 674 | 10 | US-09-899-471-2 | Sequence 2, Appl |
| 40 | 91.5 | 7.4 | 698 | 10 | US-09-899-471-5 | Sequence 5, Appl |
| 41 | 91.5 | 7.4 | 698 | 11 | US-09-866-050A-509 | Sequence 509, App |
| 42 | 91.5 | 7.4 | 698 | 11 | US-09-863-818A-8 | Sequence 8, Appl |
| 43 | 89.5 | 7.2 | 874 | 9 | US-09-818-878-26 | Sequence 26, Appl |
| 44 | 89.5 | 7.2 | 941 | 9 | US-09-818-878-47 | Sequence 47, Appl |
| 45 | 89.5 | 7.2 | 941 | 9 | US-09-211-755B-47 | Sequence 47, Appl |

ALIGNMENTS

RESULT 1
US-08-994-468-6
Sequence 6, Application US/08994468
Publication No. US20030148516A1
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for IL3/ILK-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/994,468
FILING DATE: 19-Dec-1997
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,407
FILING DATE: <unknown>
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430
TELEEX: (206) 233-0644
TELEX: 756822

SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 6:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-994-468-6

Query Match 100.0%; Score 1242; DB 7; Length 235;
Best Local Similarity 100.0%; Pred. No. 2,7e-103;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPITYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60

DB 1 MTVLAPAMSPITYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60

QY 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMGLERVNTETHEFTKCAFOPPPSCL 120

DB 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMGLERVNTETHEFTKCAFOPPPSCL 120

QY 121 REVQTNISRLQETSEOLVALKPMITRONFSKCLELQCCPDSSSTLPPWSPRPLEATAFT 180

DB 121 REVQTNISRLQETSEOLVALKPMITRONFSKCLELQCCPDSSSTLPPWSPRPLEATAFT 180

QY 181 AQPPLLILLLPVGLLLAAAMCLHMOKTRRRTPRPGQVPPVPSPODLLLVEH 235

DB 181 AQPPLLILLLPVGLLLAAAMCLHMOKTRRRTPRPGQVPPVPSPODLLLVEH 235

RESULT 2

US-09-448-378-1

Sequence 1. Application US/09448378
Patent No. US20020034517A1

GENERAL INFORMATION:
APPLICANT: Bristol, Kenneth

TITLE OF INVENTION: Dendritic Cell Stimulatory Factor

FILE REFERENCE: 2836-D

CURRENT APPLICATION NUMBER: US/09/448,378

CURRENT FILING DATE: 1999-11-23

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 1

LENGTH: 235

TYPE: PRT

ORGANISM: Homo sapiens

US-09-448-378-1

Query Match 100.0%; Score 1242; DB 9; Length 235;
Best Local Similarity 100.0%; Pred. No. 2,7e-103;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPITYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60

DB 1 MTVLAPAMSPITYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60

QY 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMGLERVNTETHEFTKCAFOPPPSCL 120

DB 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMGLERVNTETHEFTKCAFOPPPSCL 120

QY 121 REVQTNISRLQETSEOLVALKPMITRONFSKCLELQCCPDSSSTLPPWSPRPLEATAFT 180

DB 121 REVQTNISRLQETSEOLVALKPMITRONFSKCLELQCCPDSSSTLPPWSPRPLEATAFT 180

QY 181 AQPPLLILLLPVGLLLAAAMCLHMOKTRRRTPRPGQVPPVPSPODLLLVEH 235

DB 181 AQPPLLILLLPVGLLLAAAMCLHMOKTRRRTPRPGQVPPVPSPODLLLVEH 235

RESULT 3

US-09-983-806-6
Sequence 6. Application US/09983806
Patent No. US20020107365A1

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for IL13/ILK-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/983,806
FILING DATE: 25-Oct-2001

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/444,626
FILING DATE: 19-MAY-1995

APPLICATION NUMBER: US 08/762,407
FILING DATE: 03-DEC-1993

APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993

APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993

APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430

TELEEX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-983-806-6

Query Match 100.0%; Score 1242; DB 10; Length 235;
Best Local Similarity 100.0%; Pred. No. 2,7e-103;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPITYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60

DB 1 MTVLAPAMSPITYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60

QY 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMGLERVNTETHEFTKCAFOPPPSCL 120

DB 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMGLERVNTETHEFTKCAFOPPPSCL 120

QY 121 REVQTNISRLQETSEOLVALKPMITRONFSKCLELQCCPDSSSTLPPWSPRPLEATAFT 180

DB 121 REVQTNISRLQETSEOLVALKPMITRONFSKCLELQCCPDSSSTLPPWSPRPLEATAFT 180

QY 181 AQPPLLILLLPVGLLLAAAMCLHMOKTRRRTPRPGQVPPVPSPODLLLVEH 235

DB 181 AQPPLLILLLPVGLLLAAAMCLHMOKTRRRTPRPGQVPPVPSPODLLLVEH 235

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2003, 15:52:07 : Search time 25.7189 Seconds
(without alignments)
878.718 Million cell updates/sec

Title: US-09-448-378-1
Perfect score: 1242
Sequence: 1 MVLAPAMSPFTYLLLLLL.....RPGEQVPVPSPDOLLVEN 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 1242 | 100.0 | 235 | 2 | 138440 |
| 2 | 864.5 | 69.6 | 245 | 2 | S43293 |
| 3 | 834 | 67.1 | 178 | 2 | T19076 |
| 4 | 768.5 | 61.9 | 231 | 2 | A45265 |
| 5 | 606.5 | 48.8 | 220 | 2 | S43291 |
| 6 | 606.5 | 48.8 | 220 | 2 | T19076 |
| 7 | 93 | 7.5 | 1217 | 2 | T26722 |
| 8 | 92 | 7.4 | 1217 | 2 | T26722 |
| 9 | 89.5 | 7.2 | 474 | 2 | T19543 |
| 10 | 89 | 7.2 | 387 | 2 | T18201 |
| 11 | 89 | 7.2 | 793 | 1 | S60735 |
| 12 | 88.5 | 7.1 | 238 | 2 | A41990 |
| 13 | 88.5 | 7.1 | 1386 | 2 | T00257 |
| 14 | 88 | 7.1 | 753 | 2 | J00532 |
| 15 | 87.5 | 7.0 | 479 | 1 | A32290 |
| 16 | 87 | 7.0 | 910 | 2 | A53137 |
| 17 | 86.5 | 7.0 | 590 | 2 | A40437 |
| 18 | 86 | 6.9 | 299 | 2 | T17832 |
| 19 | 86 | 6.9 | 485 | 2 | A33647 |
| 20 | 86 | 6.9 | 746 | 2 | T28004 |
| 21 | 85 | 6.8 | 289 | 2 | A67646 |
| 22 | 85 | 6.8 | 366 | 2 | A37374 |
| 23 | 84 | 6.8 | 263 | 2 | T03162 |
| 24 | 84 | 6.8 | 757 | 2 | A39283 |
| 25 | 83.5 | 6.7 | 199 | 2 | A45690 |
| 26 | 83.5 | 6.7 | 530 | 2 | A45690 |
| 27 | 83 | 6.7 | 1509 | 2 | T19486 |
| 28 | 82.5 | 6.6 | 418 | 2 | T19800 |
| 29 | 82.5 | 6.6 | 426 | 2 | T36948 |

| | | | | | | |
|----|------|-----|------|---|--------|--------------------|
| 30 | 82.5 | 6.6 | 512 | 2 | D40829 | activin receptor 1 |
| 31 | 82.5 | 6.6 | 513 | 2 | J01484 | activin receptor 1 |
| 32 | 82 | 6.6 | 106 | 2 | T06479 | proline/leucine-P |
| 33 | 82 | 6.6 | 854 | 2 | T23837 | hypothetical prote |
| 34 | 81.5 | 6.6 | 485 | 2 | C75460 | hypothetical prote |
| 35 | 81.5 | 6.6 | 488 | 2 | S13423 | stromelysin 3 (EC |
| 36 | 81.5 | 6.6 | 958 | 2 | T13593 | hypothetical prote |
| 37 | 81.5 | 6.6 | 1119 | 2 | T50995 | related to cytoske |
| 38 | 81 | 6.5 | 156 | 2 | B48232 | cysteine-rich exte |
| 39 | 81 | 6.5 | 209 | 2 | A48232 | cysteine-rich exte |
| 40 | 81 | 6.5 | 294 | 2 | A12016 | hypothetical prote |
| 41 | 81 | 6.5 | 428 | 2 | S15591 | probable transposa |
| 42 | 81 | 6.5 | 488 | 2 | FHHU | Ig epsilon chain C |
| 43 | 80.5 | 6.5 | 136 | 2 | JW0047 | class I cytochrome |
| 44 | 80.5 | 6.5 | 176 | 2 | T49482 | hypothetical prote |
| 45 | 80.5 | 6.5 | 1306 | 2 | T13592 | hypothetical prote |

ALIGNMENTS

| | | | |
|--|------------------------------|--------------------------------|--------------------------|
| RESULT: 1 | 138440 | US-09-448-378-1 | human |
| C:Species: Homo sapiens (man) | C:Date: 29-May-1998 | *sequence-revision 29-May-1998 | *text-change 01-Dec-2000 |
| C:Accession: 138440 | C:Accession: 138440 | C:Accession: 138440 | C:Accession: 138440 |
| R:Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe | Blood 83, 2795-2801, 1994 | | |
| A:Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor for | | | |
| A:Reference number: 138440 | MOID:94235842 | PMID:8180375 | |
| A:Accession: 138440 | | | |
| A:Status: preliminary | translated from GB/EMBL/DBJ | | |
| A:Molecule type: mRNA | | | |
| A:Residues: 1-235 <RES> | | | |
| A:Cross-references: EMBL:U03858; NID:q494978; PIDD:AAA19825.1; PIDD:q494979 | | | |
| R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S. | Oncogene 11, 1165-1172, 1995 | | |
| A:Title: Structural analysis of human and murine flt3 ligand genomic loci. | | | |
| A:Reference number: 139075 | MOID:96032581 | PMID:7566977 | |
| A:Accession: 139075 | | | |
| A:Status: preliminary | translated from GB/EMBL/DBJ | | |
| A:Molecule type: DNA | | | |
| A:Residues: 1-235 <RES> | | | |
| A:Cross-references: EMBL:U03874; NID:q1072036; PIDD:AAA90949.1; PIDD:q1072037 | | | |
| R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; | Nature 366, 643-648, 1994 | | |
| A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoie | | | |
| A:Reference number: S43290 | MOID:94195428 | PMID:8145851 | |
| A:Accession: S43292 | | | |
| A:Status: preliminary | | | |
| A:Molecule type: mRNA | | | |
| A:Residues: 1-71, 'A', '73'-235 <HANS> | | | |
| A:Cross-references: GB:U04805; NID:q483844; PIDD:AAA17599.1; PIDD:q483845 | | | |
| A:Note: the authors translated the codon AGT for residue 25 as Met | | | |
| C:Genetics: | | | |
| A:Introns: 11/3: 48/3; 66/3; 114/3; 161/1; 226/3 | | | |

| | | | | |
|-----------------------|----------------|---|----------|------------|
| Query Match | 100.0% | Score 1242 | DB 2 | Length 235 |
| Best local similarity | 100.0% | Pred. No. 5.1e-93 | | |
| Matches 235 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY | 1 | MTVLAPAMSPFTYLLLLLLSSGLSGTQDCSPHSPISDFAAVIRELSDTLQDYPPVTV | 60 | |
| DB | 1 | MTVLAPAMSPFTYLLLLLLSSGLSGTQDCSPHSPISDFAAVIRELSDTLQDYPPVTV | 60 | |
| QY | 61 | ASNIQDEDECCGIRLVLAQRMRERKTVAGSKMGGLLEVNVRIHPTVCARPPSPSCL | 120 | |
| DB | 61 | ASNIQDEDECCGIRLVLAQRMRERKTVAGSKMGGLLEVNVRIHPTVCARPPSPSCL | 120 | |
| QY | 121 | RFVQTNISPLIOESDEVLAKPMITRONFSKCLEQCCQDSSSTLPFPPLFETAPF | 180 | |
| DB | 121 | RFVQTNISPLIOESDEVLAKPMITRONFSKCLEQCCQDSSSTLPFPPLFETAPF | 180 | |

Db 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLEIQCPDSSSTLPWPMSPPLEATAPV 180

QY 181 APQPLLILLLPVGLLLLAAMCLHMORTRRTPRPGQVPPVPSPODLLLVEH 235

Db 181 APQPLLILLLPVGLLLLAAMCLHMORTRRTPRPGQVPPVPSPODLLLVEH 235

RESULT 2

S43293

FLT3/FLK2 ligand (clone S109) - human

C:Species: Homo sapiens (man)

C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1993

C:Accession: S43293

R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kofelt, A.; Muench, M.; Kelnar, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.

A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic

A:Reference number: S43290; MUID:94195428; PMID:8145851

A:Accession: S43293

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-245 <HAN>

A:Note: the authors translated the codon AGT for residue 25 as Met

Query Match: 69.6%; Score 864.5; DB 2; Length 245;

Best Local Similarity 73.0%; Pred. No. 11e-66;

Matches 176; Conservative 7; Mismatches 27; Indels 31; Gaps 3;

QY 1 MYVLAPAMSPPTTYLLLLSSGLSTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60

Db 1 MYVLAPAMSPPTTYLLLLSSGLSTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60

QY 61 ASNLQDEELCGGLRLVLAQRMERLKTAVAGSKMOGLLELVNTEIHFTVKCAFQPPSPSC 120

Db 61 ASNLQDEELCGGLRLVLAQRMERLKTAVAGSKMOGLLELVNTEIHFTVKCAFQPPSPSC 120

QY 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLEIQCPDSSSTLPWPMSPPLEATAPV 160

Db 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLEIQCPDSSSTLPWPMSPPLEATAPV 160

QY 181 APQP-----PLLLLLPVGLLLLAAMCLHMORTRRTPRPGQVPPVSP 227

Db 178 WPRPHGEDTEAHRGESP-----ARCGIATWGRKRLARGSLIPWAPLIPSP 222

QY 228 Q 228

Db 223 E 223

RESULT 3

FLT3 ligand alternatively spliced isoform - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C:Accession: I39076

R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.

A:Title: Structural analysis of human and murine flt3 ligand genomic loci.

A:Reference number: I39075; MUID:96032581; PMID:7566377

A:Accession: I39076

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-178 <RES>

A:Cross-references: EMBL:U29874; NID:g1072036; P1DN:AAA90950.1; P1D:g1072034

C:Genetics:

A:introns: 11/3; 48/3; 66/3; 114/3; 161/1

Query Match 67.1%; Score 834; DB 2; Length 178;

Best Local Similarity 100.0%; Pred. No. 3.2e-64;

Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MYVLAPAMSPPTTYLLLLSSGLSTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60

QY 61 ASNLQDEELCGGLRLVLAQRMERLKTAVAGSKMOGLLELVNTEIHFTVKCAFQPPSPSC 120

Db 61 ASNLQDEELCGGLRLVLAQRMERLKTAVAGSKMOGLLELVNTEIHFTVKCAFQPPSPSC 120

QY 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLEIQCP 160

Db 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLEIQCP 160

RESULT 4

A49265

FLT3/FLK-2 ligand precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999

C:Accession: A49265; I49347; I49346; S43290

R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holl

D.; Williams, D.E.; Beckmann, M.P.

A:Title: Molecular cloning of a ligand for the FLT3/FLK-2 tyrosine kinase receptor: a

A:Reference number: A49265; MUID:94084751; PMID:7505204

A:Accession: A49265

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-231 <LYM>

A:Cross-references: GB:I23636; NID:g439441; P1DN:AAA9436.1; P1D:g439442

R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.

A:Title: Structural analysis of human and murine flt3 ligand genomic loci.

A:Reference number: I39075; MUID:96032581; PMID:7566377

A:Accession: I49347

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-163; 'G', '165', 'HYAG' <RES>

A:Cross-references: EMBL:U29875; NID:g1072035; P1DN:AAA90952.1; P1D:g1072041

A:Accession: I49346

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-197; 'L', '198-231' <RE2>

A:Cross-references: EMBL:U29875; NID:g1072039; P1DN:AAA90951.1; P1D:g1072040

R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Felt, A.; Muench, M.; Kelnar, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik

Nature 368, 643-648, 1994

A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic

A:Reference number: S43290; MUID:94195428; PMID:8145851

A:Accession: S43290

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-197; 'L', '198-231' <HAN>

A:Experimental source: Clone 1110

A:Note: The sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-

C:Genetics:

A:introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3

C:Keywords: transmembrane protein

Query Match 61.9%; Score 768.5; DB 2; Length 231;

Best Local Similarity 70.3%; Pred. No. 1.7e-56;

Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MYVLAPAMSPPTTYLLLLSSGLSTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 59

Db 1 MYVLAPAMSPPTTYLLLLSSGLSTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 59

QY 61 ASNLQDEELCGGLRLVLAQRMERLKTAVAGSKMOGLLELVNTEIHFTVKCAFQPPSPSC 119

Db 61 ASNLQDEELCGGLRLVLAQRMERLKTAVAGSKMOGLLELVNTEIHFTVKCAFQPPSPSC 120

QY 120 RFVOTNISRLQETSEQLVALKPWITR--QNSKCLEIQCPDSSSTLPWPMSPPLEAT 177

Db 120 RFVOTNISRLQETSEQLVALKPWITR--QNSKCLEIQCPDSSSTLPWPMSPPLEAT 177

QY 121 RFVOTNISRLQETSEQLVALKPWITR--QNSKCLEIQCPDSSSTLPWPMSPPLEAT 180

Db 121 RFVOTNISRLQETSEQLVALKPWITR--QNSKCLEIQCPDSSSTLPWPMSPPLEAT 180

QY 178 APTAPPP--LTLLLPVGLLLLAAMCLHMORTRRTPRPGQVPPVSP 227

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2003, 15:44:07 ; Search time 14.1202 seconds
(without alignments)
782.659 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242
Sequence: 1 MYLAPAWSPFTYLLLL.....RPGGVPPVSPDLLLVEN 235

Scoring table: BLOSUM62
Gap: 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|---------------|---------------------|
| 1 | 1242 | 100.0 | 235 | 1 FLJ3L_HUMAN | P49771 homo sapien |
| 2 | 768 | 61.8 | 232 | 1 FLJ3L_MOUSE | P49772 mus musculu |
| 3 | 92 | 7.4 | 661 | 1 AT12_VZVD | P09264 varicella-z |
| 4 | 90.5 | 7.3 | 5120 | 1 PCLO_CHICK | Q9PU36 gallus gall |
| 5 | 89.5 | 7.2 | 941 | 1 SGCA_HUMAN | Q75899 homo sapien |
| 6 | 89 | 7.2 | 387 | 1 SGCA_MESAU | O64255 mesocricetu |
| 7 | 89 | 7.2 | 793 | 1 S3A1_HUMAN | O15459 homo sapien |
| 8 | 87.5 | 7.0 | 415 | 1 INR3_MOUSE | P50284 mus musculu |
| 9 | 87.5 | 7.0 | 479 | 1 MPR-DROME | P20483 drosophila |
| 10 | 87 | 7.0 | 910 | 1 DDRI1_MOUSE | Q63474 rattus norv |
| 11 | 87 | 7.0 | 911 | 1 DDRI1_MOUSE | Q63474 rattus norv |
| 12 | 86.5 | 7.0 | 1394 | 1 NGC4_BOVIN | Q28181 bos taurus |
| 13 | 86 | 6.9 | 485 | 1 SSGP_VOLCA | P21997 volvox carl |
| 14 | 85 | 6.8 | 282 | 1 ATFS_HUMAN | Q9V281 homo sapien |
| 15 | 85 | 6.8 | 366 | 1 FCCN_RAT | P13599 rattus norv |
| 16 | 84.5 | 6.8 | 3726 | 1 ABF1_MOUSE | O61359 mus musculu |
| 17 | 84 | 6.8 | 592 | 1 MNT_HUMAN | Q9V563 homo sapien |
| 18 | 84 | 6.8 | 732 | 1 E4L5_HUMAN | Q9H044 homo sapien |
| 19 | 84 | 6.8 | 1234 | 1 NPHN_RAT | Q9H044 rattus norv |
| 20 | 83.5 | 6.7 | 671 | 1 2282_HUMAN | Q9H044 homo sapien |
| 21 | 83 | 6.7 | 758 | 1 VKGC_HUMAN | P38435 homo sapien |
| 22 | 82.5 | 6.6 | 334 | 1 BC12_HUMAN | Q9H049 homo sapien |
| 23 | 82 | 6.6 | 2167 | 1 SHK1_RAT | Q9H048 rattus norv |
| 24 | 81.5 | 6.6 | 488 | 1 MM11_HUMAN | P24313 homo sapien |
| 25 | 81.5 | 6.6 | 591 | 1 MNT_MOUSE | O08789 mus musculu |
| 26 | 81.5 | 6.6 | 2212 | 1 T230_HUMAN | Q93074 homo sapien |
| 27 | 81 | 6.5 | 283 | 1 ATFS_MOUSE | Q70191 mus musculu |
| 28 | 81 | 6.5 | 387 | 1 SGCA_MOUSE | P62350 mus musculu |
| 29 | 81 | 6.5 | 428 | 1 EPC_HUMAN | P01854 homo sapien |
| 30 | 81 | 6.5 | 1248 | 1 DIAT_HUMAN | O60610 homo sapien |
| 31 | 80.5 | 6.5 | 1402 | 1 IF4G_RABIT | P11110 oryctolagus |
| 32 | 80 | 6.4 | 397 | 1 CEFD_STRTL | P18549 streptomyces |
| 33 | 80 | 6.4 | 940 | 1 GBR2_RAT | O88871 rattus norv |

| | | | | | |
|----|------|-----|------|---------------|--------------------|
| 34 | 80 | 6.4 | 1174 | 1 KPC1_COCHF | Q42632 cochllobolu |
| 35 | 80 | 6.4 | 1427 | 1 ZFH2_HUMAN | Q9C0A1 homo sapien |
| 36 | 80 | 6.4 | 1794 | 1 YDC9_SCHPO | O10172 schizosacch |
| 37 | 79.5 | 6.4 | 5085 | 1 PCLO_RAT | Q9J3K6 rattus norv |
| 38 | 79 | 6.4 | 805 | 1 KIP1_YEAST | P53086 saccharomyc |
| 39 | 78.5 | 6.3 | 251 | 1 HXB4_HUMAN | P17483 homo sapien |
| 40 | 78.5 | 6.3 | 382 | 1 AVRB_RAT | P38445 rattus norv |
| 41 | 78.5 | 6.3 | 387 | 1 SGCA_RABIT | Q28686 oryctolagus |
| 42 | 78.5 | 6.3 | 401 | 1 PD61_RAT | Q94282 rattus norv |
| 43 | 78.5 | 6.3 | 913 | 1 DDRI1_HUMAN | Q68345 h epithelia |
| 44 | 78.5 | 6.3 | 1180 | 1 ATY1_HUMAN | Q9N411 homo sapien |
| 45 | 78 | 6.3 | 205 | 1 CYSR_STNY3 | Q53854 synechocyst |

ALIGNMENTS

RESULT 1
FLJ3L_HUMAN STANDARD: PRT; 235 AA.
AC P49771:
DT 01-OCT-1996 (Ref. 34, Created)
DT 01-OCT-1996 (Ref. 34, Last sequence update)
DT 25-FEB-2003 (Ref. 41, Last annotation update)
DE SL cytokine precursor (fms-related tyrosine kinase 3 ligand) (Flt3
DE ligand) (Flt3L).
GN FLT3LG.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=94195428; PubMed=8145851;
RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
RA Bazan J.F., Kastelein R., Hudak S., Wagner J., Mactson J., Lun J.,
RA Duda G., Martina N., Peterson D., Menon S., Shanafelt A.,
RA Muench M., Kelnar G., Namikawa R., Rennick D., Boncarollo M.G.,
RA Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.,
RT *Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
RT hematopoietic stem cells and is encoded by variant RNAs.*.
RL Mature 368:643-648(1994).
RN [2]
RP MEDLINE=94235842; PubMed=8160375;
RA Zeman S.D., James L., Johnson L., Brasel K., de Vries P.,
RA Escobar S.S., Downey H., Spielt R.R., Beckmann M.P., McKenna B.J.,
RT *Cloning of the human homologue of the murine flt3 ligand: a growth
RT factor for early hematopoietic progenitor cells.*.
RL Biood 83:2795-2801(1994).
RN [3]
RP MEDLINE=94032581; PubMed=7566977;
RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
RT *Structural analysis of human and murine flt3 ligand genomic loci.*;
RL Oncogene 11:1165-1172(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=20343011; PubMed=1081197;
RA Savvides S.N., Boone T., Kaipus P.A.,
RT *Flt3 ligand structure and unexpected commonalities of helical
RT bundles and cystine knots.*;
RL Nat. Struct. Biol. 7:486-491(2000).
CC -!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
CC FACTORS AND INTERLEUKINS.
CC -!- SUBUNIT: Homodimer (isoform 2).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
CC secreted (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms-2:
CC Name-1: Synonyms-Membrane-bound.

CC Isoid-P49771-1: Sequence-Displayed:
 CC Name-2: Synonyms-Soluble;
 CC Isoid-P49771-2: Sequence-VSP_004251, VSP_004252;
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
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 CC -----
 DR EMBL: 004806; AAA17999.1;
 DR EMBL: 003858; AAA19825.1;
 DR EMBL: 029874; AAA90949.1;
 DR EMBL: 029874; AAA90950.1;
 DR PIR: 138440; 138440.
 DR PIR: 139076; 139076.
 DR PDB: 1ETE; 09-JUN-00.
 DR Genew: HGNC:3766; FLT3LG.
 DR MIM: 600007;
 DR GO: 0005625; C:soluble fraction; TAS.
 DR GO: 0008284; P:positive regulation of cell proliferation; TAS.
 DR GO: 0007165; P:signal transduction; TAS.
 DR InterPro: IPR004213; FLT3_1lg.
 DR Pfam: PF02947; flt3_1lg.1.
 DR Cytokine: Glycoprotein; Transmembrane; Alternative splicing; Signal;
 KW 3D-structure.
 FT SIGNAL 1 26
 FT CHAIN 27 235
 FT DOMAIN 27 184
 FT TRANSMEM 185 205
 FT DOMAIN 206 235
 FT DISULFID 30 111
 FT DISULFID 70 153
 FT DISULFID 119 158
 FT CARBOHYD 126 126
 FT CARBOHYD 149 149
 FT VARSPLIC 161 178
 FT VARSPLIC 179 235
 FT CONFLICT 72 72
 FT STRAND 31 31
 FT TURN 39 40
 FT HELIX 41 49
 FT TURN 50 51
 FT STRAND 53 53
 FT TURN 54 55
 FT STRAND 57 61
 FT STRAND 64 64
 FT TURN 68 70
 FT HELIX 71 87
 FT TURN 88 89
 FT STRAND 90 90
 FT HELIX 92 104
 FT HELIX 106 110
 FT TURN 118 119
 FT STRAND 122 126
 FT HELIX 127 141
 FT TURN 142 147
 FT STRAND 149 149
 FT HELIX 151 153
 FT STRAND 158 158
 SQ SEQUENCE 235 AA; 26416 MW; 73995BF693B4CECF CRC64;
 Query Match 100.0%; Score 1242; DB 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 4; Se-96;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVLVAPAMSPFTYLLLLSSGLSGTQDCSFQHSPISSDFAVKTRFLSDYLQDPVTV 60
 |||

Db 1 MVLVAPAMSPFTYLLLLSSGLSGTQDCSFQHSPISSDFAVKTRFLSDYLQDPVTV 60
 QY 61 ASNZDEDELGGIMRYLAORMMERLKTAVGSKMGGILSERVNTIEHFVTKCAFQPPPSCL 120
 |||
 Db 61 ASNZDEDELGGIMRYLAORMMERLKTAVGSKMGGILSERVNTIEHFVTKCAFQPPPSCL 120
 QY 121 RPYQNTISRLLOETSEGLVALKRWTRKUNFSKCLELQOCQDSSITLPPWSPRE:EXTAPT 180
 |||
 Db 121 RPYQNTISRLLOETSEGLVALKRWTRKUNFSKCLELQOCQDSSITLPPWSPRE:EXTAPT 180
 QY 181 APOPLLILLVLVGCILLAAACIHWCKRRRTRPPRGCEVPPVPPSPDILLVEH 235
 |||
 Db 181 APOPLLILLVLVGCILLAAACIHWCKRRRTRPPRGCEVPPVPPSPDILLVEH 235
 RESULT 2
 FC3L_MOUSE
 ID FC3L_MOUSE STANDARD: PRT: 232 AA.
 AC P49772; Q64085;
 DT 01-OCT-1995 (Rel. 34, Created)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE SL_cytokine precursor (Fms-related tyrosine kinase 3 ligand) (FLT3
 DE ligand) (FLT3L).
 CN FLT3LG OR FLT3L.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 SN 11
 SEQUENCE FROM N.A.
 RX MEDLINE=94195428; PubMed=8145851;
 RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
 RA Bazan J.F., Kastelein R., Hudak S., Wagner J., Matson J., Luh J.,
 RA Duda G., Martina N., Peterson D., Menon S., Shanefelt A.,
 RA Muench M., Kelnar G., Namikawa R., Renick D., Roncarolo M.G.,
 RA Zlotnik A., Hosnet C., Dubreuil P., Birnbaum D., Lee F.;
 RT Ligand for FLT3/FLT3L receptor tyrosine kinase regulates growth of
 RT haematopoietic stem cells and is encoded by variant RNAs.";
 RL Nature 368:643-648(1994).
 RN 12
 SEQUENCE FROM N.A.
 RP STRAIN-SUI/J;
 RC MEDLINE=64084791; PubMed=7505204;
 RA Lyman S.D., James L., Vandenbos T., Devries P., Brasel K.,
 RA Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,
 RA Spielt R.R., Fletcher P.A., Maraskovsky E., Fairah T.,
 RA Foxworth D., Williams D.E., Beckmann M.P.;
 RT Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase
 RT receptor: a proliferative factor for primitive hematopoietic cells.";
 RL Cell 75:1157-1167(1993).
 RN 13
 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RP MEDL:NE-96032581; PubMed=7566977;
 RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
 RA Escobar S.;
 RT "Structural analysis of human and murine flt3 ligand genomic loci.";
 RL Oncogene 11:1165-1172(1995).
 RN 14
 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RP MEDLINE=9512470; PubMed=7824267;
 RA Lyman S.D., James L., Escobar S., Downey H., de Vries P.,
 RA Brasel K., Stocking K., Beckmann M.P., Copeland N.G.,
 RA Cleveland L.S.;
 RT Identification of soluble and membrane-bound isoforms of the murine
 RT flt3 ligand generated by alternative splicing of mRNAs.";
 RL Oncogene 10:149-157(1995).
 RN 15
 SEQUENCE FROM N.A.
 RP McClanahan T., Culpepper J., Campbell D., Wagner J.,
 RA Frenet-Bacon K., Matson J., Tsai S., Luh J., Guimares M.J.,
 RA Mantei M.-G., Rosnet O., Birnbaum D., Hannum C.;
 RL Submitted (Apr-1996) to the EMBL/GenBank/DBS databases.

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OK protein - protein search, using sw model

Run on: September 15, 2003, 15:45:12 ; Search time 62.5122 Seconds
(without alignments)
969.778 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242

Sequence: 1 MYVLAPAMSPPTTYLLILLLLL.....RPGEOYPPVPSPODLLLVEH 235

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:
2: SP bacteria:
3: SP fungi:
4: SP human:
5: SP invertebrate:
6: SP mammal:
7: SP mhc:
8: SP organelle:
9: SP phage:
10: SP plant:
11: SP rodent:
12: SP virus:
13: SP vertebrate:
14: SP unclassified:
15: SP virus:
16: SP bacteriophage:
17: SP archaea:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 895.5 | 72.1 | 294 | 6 Q9MZV0 | Q9MZV0 canis famili |
| 2 | 894.5 | 72.0 | 291 | 6 Q9MZU9 | Q9MZU9 felis silve |
| 3 | 840 | 67.6 | 292 | 6 Q9GKE0 | Q9GKE0 bos taurus |
| 4 | 835 | 67.2 | 292 | 6 Q9GKE0 | Q9GKE0 bos taurus |
| 5 | 746 | 60.1 | 274 | 6 Q9GKD9 | Q9GKD9 bos taurus |
| 6 | 602.5 | 48.5 | 172 | 11 Q61104 | Q61104 mus muscula |
| 7 | 578 | 46.5 | 169 | 11 Q9VCH4 | Q9VCH4 mus muscula |
| 8 | 112.5 | 9.1 | 579 | 10 Q9LGC8 | Q9LGC8 oryza sativ |
| 9 | 110 | 8.9 | 219 | 16 Q8DK17 | Q8DK17 synecococc |
| 10 | 105 | 8.5 | 208 | 10 Q8L418 | Q8L418 oryza sativ |
| 11 | 100.5 | 8.1 | 1809 | 11 Q8V1M6 | Q8V1M6 mus muscula |
| 12 | 97.5 | 7.9 | 669 | 10 Q8GYA4 | Q8GYA4 arabidopsis |
| 13 | 95.5 | 7.7 | 439 | 4 Q8N775 | Q8N775 homo sapien |
| 14 | 95.5 | 7.7 | 658 | 10 Q8H785 | Q8H785 arabidopsis |
| 15 | 95.5 | 7.7 | 1240 | 12 Q9DMH8 | Q9DMH8 rat cytochr |
| 16 | 93.5 | 7.5 | 658 | 10 Q9C5T0 | Q9C5T0 arabidopsis |

| | | | | | |
|----|------|-----|------|-----------|--------------------|
| 17 | 93 | 7.5 | 1217 | 5 Q17989 | Q17989 caenorhabdi |
| 18 | 92.5 | 7.4 | 387 | 11 Q8VD70 | Q8VD70 mus musculu |
| 19 | 92.5 | 7.4 | 1400 | 5 Q9YDD2 | Q9YDD2 drosophila |
| 20 | 92 | 7.4 | 251 | 4 Q9RAD2 | Q9RAD2 homo sapien |
| 21 | 91.5 | 7.4 | 287 | 16 Q8DH33 | Q8DH33 synecococc |
| 22 | 91.5 | 7.4 | 308 | 11 Q8BP15 | Q8BP15 mus musculu |
| 23 | 91.5 | 7.4 | 674 | 11 Q8K4C2 | Q8K4C2 mus musculu |
| 24 | 89.5 | 7.2 | 474 | 5 Q17610 | Q17610 caenorhabdi |
| 25 | 88.5 | 7.1 | 238 | 16 Q8YWX3 | Q8YWX3 anabena sp |
| 26 | 88.5 | 7.1 | 270 | 4 Q9JMT1 | Q9JMT1 homo sapien |
| 27 | 88.5 | 7.1 | 356 | 2 Q8KR32 | Q8KR32 yerimnia ps |
| 28 | 88.5 | 7.1 | 404 | 10 Q9AWJ4 | Q9AWJ4 oryza sativ |
| 29 | 88.5 | 7.1 | 579 | 4 Q8N158 | Q8N158 homo sapien |
| 30 | 88.5 | 7.1 | 1267 | 10 Q943D5 | Q943D5 oryza sativ |
| 31 | 88.5 | 7.1 | 1386 | 4 Q75064 | Q75064 homo sapien |
| 32 | 88 | 7.1 | 250 | 6 Q9GKE2 | Q9GKE2 sus scrofa |
| 33 | 88 | 7.1 | 753 | 12 Q56971 | Q56971 kenneya ye |
| 34 | 88 | 7.1 | 791 | 11 Q8K4Z5 | Q8K4Z5 mus musculu |
| 35 | 88 | 7.1 | 791 | 11 Q8C175 | Q8C175 mus musculu |
| 36 | 88 | 7.1 | 791 | 11 Q8C128 | Q8C128 mus musculu |
| 37 | 88 | 7.1 | 791 | 11 Q8C0M7 | Q8C0M7 mus musculu |
| 38 | 87.5 | 7.0 | 470 | 10 Q9JUI1 | Q9JUI1 arabidopsis |
| 39 | 87.5 | 7.0 | 564 | 10 Q8L729 | Q8L729 spinacia ol |
| 40 | 87.5 | 7.0 | 946 | 10 Q22015 | Q22015 cylindroche |
| 41 | 87 | 7.0 | 510 | 5 Q44018 | Q44018 leishmania |
| 42 | 87 | 7.0 | 5317 | 5 Q8TA74 | Q8TA74 hemiceurot |
| 43 | 85.5 | 7.0 | 299 | 6 Q9T7T9 | Q9T7T9 bos taurus |
| 44 | 85.5 | 7.0 | 598 | 4 Q8NHJ7 | Q8NHJ7 homo sapien |
| 45 | 86 | 6.9 | 255 | 11 Q9D3J3 | Q9D3J3 mus musculu |

ALIGNMENTS

RESULT 1
Q9MZV0 PRELIM-NARY: PRT: 294 AA.
AC Q9MZV0:
DT 01-OCT-2000 (TREMURel. 15, Created)
DT 01-OCT-2000 (TREMURel. 15, last sequence update)
DT 01-MAR-2003 (TREMURel. 23, last annotation update)
DE hit3 ligand.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
EN [1]
FP
RP
RX MEDLINE=20358731; PubMed=10902925;
RA Yang S., Sim G.K.;
RT "Molecular cloning of canine and feline hit3 ligand reveals high
RT degree of similarity to the human and mouse homologue but uniquely
RT long cytoplasmic domain".
RL DNA Seq. 11:163-166(2000).
DR EMBL: AF155148; AAF87088.1; -;
DR HSPB: P49771; IRTF.
DR InterPro: IPR004213; hit3_lig.
DR Pfam: PFD2947; hit3_lig. 1.
SC SEQUENCE 294 AA: 32394 MW: 68599178.374A3CD CRC64:

Query Match 72.1% Score 895.5; DB: 6; Length 294;
Best Local Similarity 77.1% Pred. No. 9.7e-79;
Matches 182; Conservative 12; Mismatches 35; Indels 7; Gaps 3;
QY 1 MYVLAPAMSPPTTYLLILLSSGISGTPDCSPHSPISSPFAVKRELSDYLLQDYVTV 60
DB 1 MYVLAPAMSPPTTYLLILLSSPGIKRTPDCSPHSPISSPFAVTRKLSYLLQDYVTV 60
QY 61 ASNLDELGGLMRVLAQRMRUKTVAGSKMOGLLEEVNTHIEVTYKCAFPPEPSC 120
DB 61 ASNLDELGGLMRVLAQRMRUKTVAGSKMOGLLEEVNTHIEVTYKCAFPPEPSC 120
QY 121 RFVOTNISRLQETSEQLVAKKPIKRONFSRLCLELQCCPDSSTLPPWSPRLQEARPT 160
DB 121 RFVOTNISRLQETSEQLVAKKPIKRONFSRLCLELQCCPDSSTLPPWSPRLQEARPT 160

Db 121 REVQTNISRLQTSQGLALPKWITRNFSQCLEQCPDSSSTLPVPSRPGALATAP 180
 QY 181 APQPP-LLLLLLLPVGLLLLAAMCLHWCRTRRRTPRGEVPPVPS-----PQD 229
 Db 181 APQAPLLLLLLLPAVALLMLSTAMCLHWRRRRRRSPYPGEQRTLPSERSHLPED 236

RESULT 2

Q9MZU9 PRELIMINARY: PRT: 291 AA.

AC Q9MZU9; 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, last annotation update)
 DE Flt3 ligand.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 CX NCBI_TaxID=9685;
 RN SEQUENCE FROM N.A.
 RP MEDLINE-20356731; PubMed-10902925;
 RA Yang S., Sam G.K.:
 RT Molecular cloning of canine and feline flt3 ligand reveals high
 RT degree of similarity to the human and mouse homologue but uniquely
 RT long cytoplasmic domain.*
 RL DNA Seq. 11:163-166(2000).
 DR EMBL: AF155149; AAF87089.1; -.
 DR HSSP: P49771; IETE.
 DR InterPro: IPR004213; Flt3_119.
 DR Pfam: PF02947; Flt3_119; 1.
 SQ SEQUENCE 291 AA: 32459 MW: 8F85A10A5FA0DC5 CRC64:

Query Match 72.0%; Score 894.5; DB 6; Length 291;
 Best Local Similarity 80.5%; Pred. No. 1.2e-78;
 Matches 178; Conservative 9; Mismatches 33; Indels 1; Gaps 1;

QY 1 MYLAPAWSPPTT-LLLLLLLSGLSTQDCSFQHSPISSDFAVKIRELSLYLLODPVTV 60
 Db 1 MYLAPAWSPPTT-LLLLLLLSGLSTQDCSFQHSPISSDFAVKIRELSLYLLODPVTV 60
 QY 61 ASNLQDEELCGGLWRLVLAQRWMEKLTVAAGSKMGLLRVNTLHFTVTKCAFQPPSPCL 120
 Db 61 ASNLQDEELCGGLWRLVLAQRWMEKLTVAAGSKMGLLRVNTLHFTVTKCAFQPPSPCL 120
 QY 121 REVQTNISRLQTSQGLALPKWITRNFSQCLEQCPDSSSTLPVPSRPGALATAP 180
 Db 121 REVQTNISRLQTSQGLALPKWITRNFSQCLEQCPDSSSTLPVPSRPGALATAP 180
 QY 181 APQPP-LLLLLLLPVGLLLLAAMCLHWCRTRRRTPRGEQ 220
 Db 181 APQAPLLLLLLLPAVALLMLSTAMCLHWRRRRRRSPYPGEQ 221

RESULT 3

Q9GKEO PRELIMINARY: PRT: 292 AA.

AC Q9GKEO; 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, last annotation update)
 DE Flt3 ligand isoform-1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 CX NCBI_TaxID=9913;
 RN SEQUENCE FROM N.A.
 RP MEDLINE-20570936; PubMed-11120823;
 RA Wang W., Brown W.C., Palmer G.H.:
 RT Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain

RT required for receptor binding and function using naturally occurring
 RT ligand isoforms.*
 RL J. Immunol. 165:6966-6974(2000).
 DR EMBL: AF282985; AAF99322.1; -.
 DR HSSP: P49771; IETE.
 DR InterPro: IPR004213; Flt3_119.
 DR Pfam: PF02947; Flt3_119; 1.
 SQ SEQUENCE 292 AA: 32390 MW: D68B9ED79221202D CRC64:

Query Match 67.6%; Score 840; DB 6; Length 292;
 Best Local Similarity 76.3%; Pred. No. 2.3e-73;
 Matches 171; Conservative 12; Mismatches 37; Indels 4; Gaps 2;

QY 1 MYLAPAWSPPTT-LLLLLLLSGLSTQDCSFQHSPISSDFAVKIRELSLYLLODPVTV 59
 Db 1 MYLAPAWSPPTT-LLLLLLLSGLSTQDCSFQHSPISSDFAVKIRELSLYLLODPVTV 60
 QY 60 VASNLQDEELCGGLWRLVLAQRWMEKLTVAAGSKMGLLRVNTLHFTVTKCAFQPPSPCL 119
 Db 61 VASNLQDEELCGGLWRLVLAQRWMEKLTVAAGSKMGLLRVNTLHFTVTKCAFQPPSPCL 120
 QY 120 REVQTNISRLQTSQGLALPKWITRNFSQCLEQCPDSSSTLPVPSRPGALATAP 179
 Db 120 REVQTNISRLQTSQGLALPKWITRNFSQCLEQCPDSSSTLPVPSRPGALATAP 180
 QY 180 APQPP-LLLLLLLPVGLLLLAAMCLHWCRTRRRTPRGEQ 220
 Db 181 PGQSPLLLLLLLPAVALLMLSTAMCLHWRRRRRRSPYPGER 224

RESULT 4

Q8NMW1 PRELIMINARY: PRT: 292 AA.

AC Q8NMW1; 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, last annotation update)
 DE Flt3 ligand.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 CX NCBI_TaxID=9913;
 RN SEQUENCE FROM N.A.
 RP Hiko H., Momotani E.:
 RT "Cloning of a cDNA for bovine flt3 ligand.";
 RT Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB051841; BAB79634.1; -.
 DR InterPro: IPR004213; Flt3_119.
 DR Pfam: PF02947; Flt3_119; 1.
 SQ SEQUENCE 292 AA: 32388 MW: 2A797E0C1199C1D9 CRC64:

Query Match 67.2%; Score 835; DB 6; Length 292;
 Best Local Similarity 75.9%; Pred. No. 7.1e-73;
 Matches 170; Conservative 12; Mismatches 38; Indels 4; Gaps 2;

QY 1 MYLAPAWSPPTT-LLLLLLLSGLSTQDCSFQHSPISSDFAVKIRELSLYLLODPVTV 59
 Db 1 MYLAPAWSPPTT-LLLLLLLSGLSTQDCSFQHSPISSDFAVKIRELSLYLLODPVTV 60
 QY 60 VASNLQDEELCGGLWRLVLAQRWMEKLTVAAGSKMGLLRVNTLHFTVTKCAFQPPSPCL 119
 Db 61 VASNLQDEELCGGLWRLVLAQRWMEKLTVAAGSKMGLLRVNTLHFTVTKCAFQPPSPCL 120
 QY 120 REVQTNISRLQTSQGLALPKWITRNFSQCLEQCPDSSSTLPVPSRPGALATAP 179
 Db 120 REVQTNISRLQTSQGLALPKWITRNFSQCLEQCPDSSSTLPVPSRPGALATAP 180
 QY 180 APQPP-LLLLLLLPVGLLLLAAMCLHWCRTRRRTPRGEQ 220
 Db 181 PGQSPLLLLLLLPAVALLMLSTAMCLHWRRRRRRSPYPGER 224

PR 12-AUG-1993: 93US-0106463.
 PR 25-AUG-1993: 93US-0111758.
 PR 03-DEC-1993: 93US-0162407.
 PR 07-MAR-1994: 94US-0209502.
 PR 11-MAY-1994: 94US-0243545.
 XX
 PA (IMMV) IMMUNEX CORP.
 PI Beckmann MP, Lyman SD:
 XX
 DR WPI: 1995-008971/02.
 DR N-PSDB: AAO79076.
 XX
 PT Isolated ligands for flt 3 receptors - useful for treating
 PT anaemia, AIDS and various cancers
 XX
 PS Disclosure: Page 25-27: 33pp: English.
 XX
 CC CDNA encoding mouse flt3 ligand (flt3-L) was isolated from a
 CC CDNA library of T-cell line P7B-0.3M in CV-1/EBNA-1 cells
 CC using a slide autoradiography method. flt3-L stimulates
 CC production of progenitor and stem cells, and can be used e.g.
 CC in gene therapy protocols.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 231 AA:
 Query Match 100.0%: Score 1223: DB 16: Length 231:
 Best Local Similarity 100.0%: Pred. No. 5.5e-115:
 Matches 231: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKYKFKELTDHLKDPVT 60
 DB 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKYKFKELTDHLKDPVT 60
 QY 61 VAVNLQDEKCKALMSFLAQRMIQKTVAGSKMOTLEDVNTETIHVYISCTOPLEPC 120
 DB 61 VAVNLQDEKCKALMSFLAQRMIQKTVAGSKMOTLEDVNTETIHVYISCTOPLEPC 120
 QY 121 LRFVQINISHLKDTQTLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
 DB 121 LRFVQINISHLKDTQTLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
 QY 181 ELPEPRRQRLLLLLLPLTLVLLAAAGLKWQARRRGELHGVPLPSHP 231
 DB 181 ELPEPRRQRLLLLLLPLTLVLLAAAGLKWQARRRGELHGVPLPSHP 231
 RESULT 2
 AAM67768
 ID AAM67768 standard: Protein: 231 AA.
 XX
 AC AAM67768:
 XX
 DT 25-MAR-1999 (first entry)
 XX
 DE Murine flt3-ligand.
 XX
 KM Antigen-specific peripheral immune tolerance: flt3-ligand: flt3-L;
 KM immunogenic: autoimmune disease: organ transplantation: food allergy;
 KM tissue transplantation.
 XX
 OS Mus sp.
 XX
 PN MO9857655-A1.
 XX
 PD 23-DEC-1998.
 XX
 PF 12-JUN-1998: 98MO-US12085.
 XX
 PR 17-JUN-1997: 97US-0877421.
 XX
 PA (IMMV) IMMUNEX CORP.

XX
 PT Abbott NM, Mowat AM, Viney JL:
 XX
 DR WPI: 1999-070422/06.
 DR N-PSDB: AAV81505.
 XX
 PT Methods for initiating or enhancing antigen specific immune
 PT tolerance - by using murine or human flt3 ligand
 XX
 PS Claim 1: Page 12: 25pp: English.
 XX
 CC A method has been developed of initiating or enhancing: (i) an antigen-
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic
 CC immunogenic molecule by addition of a polypeptide, before, after or with
 CC the mucosal administration of an immunotolerising amount of the antigen
 CC or therapeutic molecule, respectively. The polypeptide is capable of
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino
 CC acids 28-y of human flt3-L, where y is an amino acid between 163-235;
 CC and c) a polypeptide that has at least 90% identity to the polypeptides
 CC of either (a) or (b). The method ameliorates the effects of autoimmune
 CC diseases, food allergies or organ or tissue rejection following
 CC transplantation. Administration of flt3-L allows lower doses of antigens
 CC to be used in vivo for mucosally administered antigens. The present
 CC sequence represents murine flt3-L.
 CC
 XX
 SQ Sequence 231 AA:
 Query Match 100.0%: Score 1223: DB 20: Length 231:
 Best Local Similarity 100.0%: Pred. No. 5.5e-115:
 Matches 231: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKYKFKELTDHLKDPVT 60
 DB 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKYKFKELTDHLKDPVT 60
 QY 61 VAVNLQDEKCKALMSFLAQRMIQKTVAGSKMOTLEDVNTETIHVYISCTOPLEPC 120
 DB 61 VAVNLQDEKCKALMSFLAQRMIQKTVAGSKMOTLEDVNTETIHVYISCTOPLEPC 120
 QY 121 LRFVQINISHLKDTQTLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
 DB 121 LRFVQINISHLKDTQTLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
 QY 181 ELPEPRRQRLLLLLLPLTLVLLAAAGLKWQARRRGELHGVPLPSHP 231
 DB 181 ELPEPRRQRLLLLLLPLTLVLLAAAGLKWQARRRGELHGVPLPSHP 231
 RESULT 3
 AAB20186
 ID AAB20186 standard: Protein: 231 AA.
 XX
 AC AAB20186:
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Mouse flt3 ligand.
 XX
 KM flt3 ligand: Fms-like tyrosine kinase: mouse; vaccine;
 KM immunotherapy: therapy: tumour; cancer; melanoma; glioma;
 KM lymphoma; autoimmune disease: infection; gene therapy.
 XX
 OS Mus musculus.
 XX
 PN
 XX
 PD
 XX
 PF
 XX
 PR
 XX
 PA Domain
 Location/Qualifiers
 1..27
 /label=Signal_peptide
 28..231
 /label=Mature_protein
 28..189
 /label=Extracellular_domain
 189..231

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2003, 15:52:22 : Search time 20.324 Seconds
(without alignments)
480.899 Million cell updates/sec

Title: US-09-448-378-2
1223
Sequence: 1 MTVALPAMSPNSLLLLLL.....MQRARRGELHPGVLPSP 231

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCrus_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------|------------------|
| 1 | 1223 | 100.0 | 231 | 1 | US-08-243-545-2 |
| 2 | 1223 | 100.0 | 231 | 2 | US-08-993-962-2 |
| 3 | 1223 | 100.0 | 231 | 3 | US-09-160-841-2 |
| 4 | 1223 | 100.0 | 231 | 5 | PCT-US94-05365-2 |
| 5 | 1220 | 99.8 | 231 | 1 | US-08-220-3798-7 |
| 6 | 1220 | 99.8 | 231 | 1 | PCT-US94-03866-6 |
| 7 | 774 | 63.3 | 294 | 4 | US-09-322-409-7 |
| 8 | 774 | 63.3 | 294 | 4 | US-09-451-527-7 |
| 9 | 768.5 | 62.8 | 235 | 1 | US-08-243-545-6 |
| 10 | 768.5 | 62.8 | 235 | 2 | US-08-993-962-6 |
| 11 | 768.5 | 62.8 | 235 | 3 | US-09-160-841-6 |
| 12 | 768.5 | 62.8 | 235 | 3 | US-09-109-100-1 |
| 13 | 768.5 | 62.8 | 235 | 5 | PCT-US94-05365-6 |
| 14 | 761 | 62.2 | 291 | 4 | US-09-322-409-44 |
| 15 | 761 | 62.2 | 291 | 4 | US-09-451-527-44 |
| 16 | 724.5 | 59.2 | 137 | 4 | US-09-109-100-19 |
| 17 | 692 | 56.6 | 212 | 3 | US-09-109-100-10 |
| 18 | 687 | 56.2 | 209 | 3 | US-09-109-100-15 |
| 19 | 686 | 56.1 | 209 | 3 | US-09-109-100-14 |
| 20 | 686 | 56.1 | 209 | 3 | US-09-109-100-18 |
| 21 | 685 | 56.0 | 209 | 3 | US-09-109-100-16 |
| 22 | 682 | 55.8 | 209 | 3 | US-09-109-100-9 |
| 23 | 682 | 55.8 | 209 | 3 | US-09-109-100-12 |
| 24 | 682 | 55.8 | 209 | 3 | US-09-109-100-17 |
| 25 | 680 | 55.6 | 209 | 3 | US-09-109-100-11 |
| 26 | 679.5 | 55.6 | 209 | 4 | US-09-322-409-23 |
| 27 | 679.5 | 55.6 | 268 | 4 | US-09-451-527-23 |

| | | | | | | |
|----|-------|------|-----|---|--------------------|-------------------|
| 28 | 679 | 55.5 | 209 | 3 | US-09-109-100-13 | Sequence 13, Appl |
| 29 | 678 | 55.4 | 209 | 3 | US-09-109-100-8 | Sequence 8, Appl |
| 30 | 668 | 54.6 | 276 | 4 | US-09-322-409-26 | Sequence 26, Appl |
| 31 | 668 | 54.6 | 276 | 4 | US-09-451-527-26 | Sequence 26, Appl |
| 32 | 666.5 | 54.5 | 265 | 4 | US-09-322-409-49 | Sequence 49, Appl |
| 33 | 666.5 | 54.5 | 265 | 4 | US-09-451-527-49 | Sequence 49, Appl |
| 34 | 573.5 | 46.9 | 250 | 4 | US-09-322-409-11 | Sequence 31, Appl |
| 35 | 573.5 | 46.9 | 250 | 4 | US-09-451-527-11 | Sequence 31, Appl |
| 36 | 216 | 17.7 | 42 | 5 | PCT-US94-05150-17 | Sequence 17, Appl |
| 37 | 135 | 11.0 | 28 | 5 | PCT-US94-05150-12 | Sequence 12, Appl |
| 38 | 105 | 8.6 | 22 | 5 | PCT-US94-05150-10 | Sequence 10, Appl |
| 39 | 95.5 | 7.8 | 909 | 2 | US-08-310-912A-142 | Sequence 142, App |
| 40 | 95.5 | 7.8 | 909 | 3 | US-09-301-085-142 | Sequence 142, App |
| 41 | 95.5 | 7.8 | 909 | 5 | PCT-US95-04589-142 | Sequence 142, App |
| 42 | 92 | 7.5 | 885 | 2 | US-08-310-912A-2 | Sequence 2, Appl |
| 43 | 92 | 7.5 | 885 | 3 | US-09-841-089-2 | Sequence 2, Appl |
| 44 | 92 | 7.5 | 885 | 3 | US-09-101-085-2 | Sequence 2, Appl |
| 45 | 92 | 7.5 | 885 | 5 | PCT-US95-04570-2 | Sequence 2, Appl |

ALIGNMENTS

RESULT 1
US-08-243-545-2
Sequence 2, Application US/08243545
Patent No. 554512
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for Flt3/Tk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 5, University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-243-545-2

Query Match 100.0%; Score 1223; DB 1; Length 231;
Best Local Similarity 100.0%; Pred. No. 7.7e-119;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYSHSPSSNFKVRFRELDHLKDYVAT 60
DB 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYSHSPSSNFKVRFRELDHLKDYVAT 60
QY 61 VAVNLODEKHKALMSLEFLAQRWIEQLKTVAGSKMOTLLEDVNTETHEVTSCTFQPLPEC 120
DB 61 VAVNLODEKHKALMSLEFLAQRWIEQLKTVAGSKMOTLLEDVNTETHEVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQQLLLILLPLTLVLLAAAGLRWQARRRGELHPGVPLPSHP 231
DB 181 ELPEPRRQQLLLILLPLTLVLLAAAGLRWQARRRGELHPGVPLPSHP 231

RESULT 2
US-08-993-962-2
Sequence 2, Application US/08993962
Patent No. 5843423

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,962
FILING DATE: December 18, 1997
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758

CLASSIFICATION: 424
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463

CLASSIFICATION: 424
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394

ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-448-378-2

Query Match 100.0%; Score 1223; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 7.7e-119;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYSHSPSSNFKVRFRELDHLKDYVAT 60
DB 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYSHSPSSNFKVRFRELDHLKDYVAT 60
QY 61 VAVNLODEKHKALMSLEFLAQRWIEQLKTVAGSKMOTLLEDVNTETHEVTSCTFQPLPEC 120
DB 61 VAVNLODEKHKALMSLEFLAQRWIEQLKTVAGSKMOTLLEDVNTETHEVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQQLLLILLPLTLVLLAAAGLRWQARRRGELHPGVPLPSHP 231
DB 181 ELPEPRRQQLLLILLPLTLVLLAAAGLRWQARRRGELHPGVPLPSHP 231

RESULT 3
US-09-60-841-2
Sequence 2, Application US/09160841
Patent No. 6190655

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,841
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993

APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463

CLASSIFICATION: 424
FILING DATE: May 24, 1993
APPLICATION NUMBER: 08/068,394

ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: September 15, 2003, 15:57:23 : Search time 39.6567 Seconds
(without alignments)
849.940 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223

Sequence: 1 MVTAPAMSPNSLLLL.....MORARRGELHGVLPSPSP 231

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications.AA.*
2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/PCV_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being plotted,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
| 1 | 1223 | 100.0 | 231 | 7 | US-08-994-468-2 |
| 2 | 1223 | 100.0 | 231 | 9 | US-09-448-378-2 |
| 3 | 1223 | 100.0 | 231 | 10 | US-09-983-806-2 |
| 4 | 1223 | 100.0 | 231 | 12 | US-10-314-035-2 |
| 5 | 1223 | 100.0 | 231 | 14 | US-10-095-449-2 |
| 6 | 774 | 63.3 | 234 | 12 | US-10-262-439-7 |
| 7 | 774 | 63.3 | 234 | 15 | US-10-218-654-7 |
| 8 | 768.5 | 62.8 | 235 | 9 | US-08-994-468-6 |
| 9 | 768.5 | 62.8 | 235 | 9 | US-09-448-378-1 |
| 10 | 768.5 | 62.8 | 235 | 10 | US-09-983-806-6 |
| 11 | 768.5 | 62.8 | 235 | 10 | US-09-904-536-1 |
| 12 | 768.5 | 62.8 | 235 | 12 | US-10-314-035-6 |
| 13 | 768.5 | 62.8 | 235 | 14 | US-10-095-449-6 |
| 14 | 768.5 | 62.8 | 235 | 15 | US-10-241-927-2 |
| 15 | 761 | 62.2 | 291 | 12 | US-10-262-439-44 |

| | | | | | | |
|----|-------|------|-----|----|--------------------|-------------------|
| 16 | 761 | 62.2 | 291 | 15 | US-10-218-654-44 | Sequence 44, Appl |
| 17 | 724.5 | 59.2 | 137 | 10 | US-09-904-536-19 | Sequence 19, Appl |
| 18 | 592 | 56.6 | 212 | 10 | US-09-904-536-10 | Sequence 10, Appl |
| 19 | 687 | 56.2 | 209 | 10 | US-09-904-536-15 | Sequence 15, Appl |
| 20 | 686 | 56.1 | 209 | 10 | US-09-904-536-14 | Sequence 14, Appl |
| 21 | 686 | 56.1 | 209 | 10 | US-09-904-536-18 | Sequence 18, Appl |
| 22 | 685 | 56.0 | 209 | 10 | US-09-904-536-16 | Sequence 16, Appl |
| 23 | 682 | 55.8 | 209 | 10 | US-09-904-536-9 | Sequence 9, Appl |
| 24 | 682 | 55.8 | 209 | 10 | US-09-904-536-12 | Sequence 12, Appl |
| 25 | 682 | 55.8 | 209 | 10 | US-09-904-536-17 | Sequence 17, Appl |
| 26 | 680 | 55.6 | 209 | 10 | US-09-904-536-11 | Sequence 11, Appl |
| 27 | 679.5 | 55.6 | 268 | 12 | US-10-262-439-23 | Sequence 23, Appl |
| 28 | 679.5 | 55.6 | 268 | 15 | US-10-218-654-23 | Sequence 23, Appl |
| 29 | 679 | 55.5 | 209 | 10 | US-09-904-536-13 | Sequence 13, Appl |
| 30 | 678 | 55.4 | 209 | 10 | US-09-904-536-6 | Sequence 8, Appl |
| 31 | 668 | 54.6 | 276 | 12 | US-10-262-439-26 | Sequence 26, Appl |
| 32 | 668 | 54.6 | 276 | 15 | US-10-218-654-26 | Sequence 26, Appl |
| 33 | 666.5 | 54.5 | 265 | 12 | US-10-262-439-49 | Sequence 49, Appl |
| 34 | 666.5 | 54.5 | 265 | 15 | US-10-218-654-49 | Sequence 49, Appl |
| 35 | 573.5 | 46.9 | 250 | 12 | US-10-262-439-31 | Sequence 31, Appl |
| 36 | 573.5 | 46.9 | 250 | 15 | US-10-218-654-31 | Sequence 31, Appl |
| 37 | 562 | 46.4 | 156 | 15 | US-10-053-355A-1 | Sequence 1, Appl |
| 38 | 95.5 | 7.8 | 909 | 10 | US-09-867-852-142 | Sequence 142, App |
| 39 | 94 | 7.7 | 355 | 10 | US-09-948-018-2 | Sequence 2, Appl |
| 40 | 92 | 7.5 | 885 | 10 | US-09-867-852-2 | Sequence 2, Appl |
| 41 | 91.5 | 7.5 | 941 | 15 | US-10-225-567A-436 | Sequence 435, App |
| 42 | 89.5 | 7.3 | 874 | 9 | US-09-826-508-26 | Sequence 26, Appl |
| 43 | 89.5 | 7.3 | 941 | 9 | US-09-818-879-47 | Sequence 47, Appl |
| 44 | 89.5 | 7.3 | 941 | 9 | US-09-211-755B-47 | Sequence 47, Appl |
| 45 | 89.5 | 7.3 | 941 | 10 | US-09-793-139-47 | Sequence 47, Appl |

ALIGNMENTS

RESULT 1
US-08-994-468-2
: Sequence 2, Appl: US-08-994-468
: Pub: Application No. US20030148516A1
: GENERAL INFORMATION:
: APPLICANT: Lyman, Stewart D.
: Beckmann, M. Patricia
: TITLE OF INVENTION: Ligands for fliA/fliK-2 Receptors
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Stephen L. Malaska, Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: Washington
: COUNTRY: US
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Macintosh 7.0
: SOFTWARE: Microsoft Word, Version 45.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/994,468
: FILING DATE: 19-Dec-1997
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/162,407
: FILING DATE: <Unknown>
: APPLICATION NUMBER: 08/111,758
: FILING DATE: August 25, 1993
: APPLICATION NUMBER: 08/106,463
: FILING DATE: August 12, 1993
: APPLICATION NUMBER: 08/058,394
: FILING DATE: May 24, 1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Malaska, Stephen L.
: REGISTRATION NUMBER: 32,655
: REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 231 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-08-994-468-2

Query Match 100.0%; Score 1223; DB 7; Length 231;

Best Local Similarity 100.0%; Pred. No. 2, 1e-108;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVKFRELTDHLKDYPT 60

DB 1 MTVLAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVKFRELTDHLKDYPT 60

QY 61 VAVNLODEKCKALMSFLAQRWIEQLKTVAGSKMOTLLLEDVNTLHFVTSCFOPLPFC 120

DB 61 VAVNLODEKCKALMSFLAQRWIEQLKTVAGSKMOTLLLEDVNTLHFVTSCFOPLPFC 120

QY 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPTALEAT 180

DB 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPTALEAT 180

QY 181 ELPEPRRQRLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

DB 181 ELPEPRRQRLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

QY 131 ELPEPRRQRLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

DB 131 ELPEPRRQRLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

QY 181 ELPEPRRQRLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

DB 181 ELPEPRRQRLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

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QY 181 ELPEPRRQRLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

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DB 181 ELPEPRRQRLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

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DB 181 ELPEPRRQRLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

QY 181 ELPEPRRQRLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

RESULT 3

US-09-983-806-2

Sequence 2, Application US/09983805

Patent No. US20020107365A1

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.

Beckmann, M. Patricia

TITLE OF INVENTION: Ligands for F113/LK-2 Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESS: Stephen L. Malaska, Immunex Corporation

SUBJECT: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0.1

SOFTWARE: Microsoft Word, Version 4.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/983,805

FILING DATE: 25-Oct-2001

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/444,625

FILING DATE: 19-MAY-1995

APPLICATION NUMBER: US 08/162,407

FILING DATE: 03-DEC-1993

APPLICATION NUMBER: 08/111,758

FILING DATE: August 25, 1993

APPLICATION NUMBER: 08/106,463

FILING DATE: August 12, 1993

APPLICATION NUMBER: 08/068,394

FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 28-3-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 231 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-983-806-2

Query Match 100.0%; Score 1223; DB 10; Length 231;

Best Local Similarity 100.0%; Pred. No. 2, 1e-108;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVKFRELTDHLKDYPT 60

DB 1 MTVLAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVKFRELTDHLKDYPT 60

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DB 61 VAVNLODEKCKALMSFLAQRWIEQLKTVAGSKMOTLLLEDVNTLHFVTSCFOPLPFC 120

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DB 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPTALEAT 180

QY 181 ELPEPRRQRLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

DB 181 ELPEPRRQRLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2003, 15:52:07 : Search time 25.2811 seconds
(without alignments)
878.718 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223

Sequence: 1 MTVLAPAMSPNSLLLLLL.....MQBARRRGELHPGVPLPSHP 231

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 1223 | 100.0 | 231 | 2 A49265 | flt3/Flt3-2 ligand |
| 2 | 879 | 71.9 | 220 | 2 S43291 | FLT3/FLK2 ligand |
| 3 | 879 | 71.9 | 220 | 2 I58343 | flt3 ligand isolet |
| 4 | 768.5 | 62.8 | 235 | 2 I38440 | flt3 ligand - huma |
| 5 | 616.5 | 50.4 | 245 | 2 S43293 | FLT3/FLK2 ligand |
| 6 | 594.5 | 48.6 | 178 | 2 I39076 | FLT3 ligand altera |
| 7 | 95.5 | 7.8 | 909 | 1 A54809 | disease resistance |
| 8 | 88 | 7.2 | 843 | 2 T01438 | hypothetical prote |
| 9 | 87 | 7.1 | 291 | 2 AFO123 | probable antiscric |
| 10 | 86 | 7.0 | 962 | 2 T31617 | SERA antigen/papa |
| 11 | 85 | 7.0 | 181 | 2 T20323 | hypothetical prote |
| 12 | 84.5 | 6.9 | 939 | 2 E82121 | peptidase, insulin |
| 13 | 84 | 6.9 | 1409 | 2 T37188 | presynaptic activ |
| 14 | 83.5 | 6.8 | 552 | 1 A31401 | macrophage colony- |
| 15 | 83.5 | 6.8 | 552 | 1 S35703 | colony-stimulating |
| 16 | 83.5 | 6.8 | 2476 | 2 T34022 | zonadhesin - pig |
| 17 | 82.5 | 6.7 | 378 | 2 S00842 | leukostallin precu |
| 18 | 82.5 | 6.7 | 431 | 2 T04868 | hypothetical prote |
| 19 | 81 | 6.6 | 4131 | 2 T12085 | hypothetical prote |
| 20 | 80.5 | 6.6 | 391 | 2 B40892 | apolipoprotein A-I |
| 21 | 80.5 | 6.6 | 394 | 2 A25281 | apolipoprotein A-I |
| 22 | 80.5 | 6.6 | 395 | 2 A40892 | apolipoprotein A-I |
| 23 | 80 | 6.5 | 382 | 2 E84527 | hypothetical prote |
| 24 | 79.5 | 6.5 | 399 | 2 C40892 | apolipoprotein A-I |
| 25 | 79.5 | 6.5 | 745 | 2 T38299 | apolipoprotein A-I |
| 26 | 79.5 | 6.5 | 1101 | 2 S58108 | probable beta-adap |
| 27 | 78.5 | 6.4 | 122 | 2 D70730 | hypothetical prote |
| 28 | 78.5 | 6.4 | 315 | 2 T24821 | hypothetical prote |
| 29 | 78.5 | 6.4 | 379 | 2 T11349 | ubiquitin-cytocaro |

| | | | | | |
|----|------|-----|------|----------|--------------------|
| 30 | 78.5 | 6.4 | 468 | 2 T23091 | hypothetical prote |
| 31 | 78.5 | 6.4 | 3668 | 1 A44962 | genome polyprotein |
| 32 | 78 | 6.4 | 224 | 2 I37243 | CMRF-35 antigen |
| 33 | 78 | 6.4 | 243 | 2 I34632 | probable bi-functi |
| 34 | 78 | 6.4 | 806 | 2 E64221 | phenylalanine-tRNA |
| 35 | 78 | 6.4 | 508 | 2 S51293 | probable membrane |
| 36 | 78 | 6.4 | 1601 | 2 AE2011 | hypothetical prote |
| 37 | 78 | 6.4 | 1715 | 2 T06145 | disease resistance |
| 38 | 77.5 | 6.3 | 266 | 2 A45844 | MHC class II histo |
| 39 | 77.5 | 6.3 | 456 | 2 B72130 | frame-shift with c |
| 40 | 77.5 | 6.3 | 579 | 2 JC7629 | membrane-type fliz |
| 41 | 77.5 | 6.3 | 746 | 2 S67203 | probable membrane |
| 42 | 77.5 | 6.3 | 774 | 2 B86492 | hypothetical prote |
| 43 | 77.5 | 6.3 | 774 | 2 H81540 | hypothetical prote |
| 44 | 77.5 | 6.3 | 811 | 2 E72003 | hypothetical prote |
| 45 | 77 | 6.3 | 619 | 2 D86509 | S/T protein kinase |

ALIGNMENTS

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RESULT 1
A49265
flt3/Flt3-2 ligand precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence-revision 13-Jan-1995 #text-change DB-Oct-1999
C:Accession: A49265; 149347; 149346; S43290
R:Lyman, S.D.; James, L.; Vander Bos, T.; de Vries, P.; Braset, K.; Giniak, B.; Holl
E.; Williams, D.E.; Beckmann, M.P.
Cell 75, 1157-1167, 1993
A:Title: Molecular cloning of a ligand for the flt3/Flt3-2 tyrosine kinase receptor: a
A:Reference number: A49265; MUID:54C84791; PKID:7505204
A:Accession: A49265
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-231 <LYN>
A:Cross-references: GR:123636; NID:G439441; PIDN:AA439436.1; PID:G439442
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Growth 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: 139075; MUID:96032581; PMID:7565977
A:Accession: 149347
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-163; 'G', 165, 'TRAC' <RES>
A:Cross-references: EMBL:U29875; NID:q1072039; PIDN:AA50952.1; PID:q1072041
A:Accession: 149346
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-197; 'C', 198-231 <RE2>
A:Cross-references: EXBL:U29875; NID:q1072039; PIDN:AA50951.1; PID:q1072040
R:Hamum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;
felt, A.; Mench, M.; Kohner, G.; Namioka, K.; Rennick, D.; Roncarolo, M.G.; Zlotnik
Nature 368, 643-648, 1994
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic
A:Reference number: S43290; MUID:94195428; PMID:8145951
A:Accession: S43290
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-197; 'L', 198-231 <HAN>
A:Experimental source: clone T110
A:Note: the sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-
C:Genetics:
A:introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3
C:Keywords: transmembrane protein

Query Match 100.0%; Score 1223; DB 2; Length 231;
Best Local Similarity 100.0%; Prod. No. 3.4e-101;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 MTVLAPAMSPNSLLLLLLSPCLRGTPDCYFSHPSSNFKYKPRELTHLLKDPVT 60
|||||
1 MTVLAPAMSPNSLLLLLLSPCLRGTPDCYFSHPSSNFKYKPRELTHLLKDPVT 60
ubiquitin-cytocaro

```

QY 61 VAVNLODEKHKALMSLFLAORMIEOLKTVAGSKMOTLLEEDVTEIHFTVSCFQPLPEC 120
 Db 61 VAVNLODEKHKALMSLFLAORMIEOLKTVAGSKMOTLLEEDVTEIHFTVSCFQPLPEC 120
 QY 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNSRCLEVOCCPDSSTLLPPRSPLAEAT 180
 Db 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNSRCLEVOCCPDSSTLLPPRSPLAEAT 180
 QY 181 ELPEPPRROLULLLLPLTLVLLAAAMGLRMORARRGELHGVLPSP 231
 Db 181 ELPEPPRROLULLLLPLTLVLLAAAMGLRMORARRGELHGVLPSP 231

RESULT 2

FLIT3/PLK2 ligand (clone T118) - mouse
 S43291
 C:Species: Mus musculus (house mouse)
 C>Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
 C:Accession: S43291
 R:Hanum, S.D.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; K
 felt, A.; Muench, M.; Kelnier, G.; Nankawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
 Nature 368, 643-648, 1994
 A:Title: Ligand for FLIT3/PLK2 receptor tyrosine kinase regulates growth of haematopoietic
 A:Reference number: S43290; MUID:94195428; PMID:8145851
 A:Accession: S43291
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-220 <HMAN>

Query Match 71.9%; Score 879; DB 2; Length 220;
 Best Local Similarity 82.3%; Pred. No. 1, 1e-70;
 Matches 177; Conservative 5; Mismatches 21; Indels 12; Gaps 3;

QY 1 MTVLAPAMSPNSLLLLLSPLCRGTGTCYFSSHPISNFKVKFRELTHLXDPVT 60
 Db 1 MTVLAPAMSPNSLLLLLSPLCRGTGTCYFSSHPISNFKVKFRELTHLXDPVT 60
 QY 61 VAVNLODEKHKALMSLFLAORMIEOLKTVAGSKMOTLLEEDVTEIHFTVSCFQPLPEC 120
 Db 61 VAVNLODEKHKALMSLFLAORMIEOLKTVAGSKMOTLLEEDVTEIHFTVSCFQPLPEC 120
 QY 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNSRCLEVOCCPDSSTLLPPRSPLAEAT 180
 Db 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNSRCLEVOCCPDSSTLLPPRSPLAEAT 180
 QY 177 LEATLEPPRRROLULL-----LLPLTLVLLAA 206
 Db 178 LTAATALLVCQGLLPLVGTSHMFFLPYFLSPSS 212

RESULT 3

FLIT3 ligand isoform 5H - mouse
 S43291
 C:Species: Mus sp. (mouse)
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
 C:Accession: S43291
 R:Hanum, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Stocking, S.
 Oncogene 10, 149-157, 1995
 A:Title: Identification of soluble and membrane-bound isoforms of the murine FLIT3 ligand
 A:Reference number: S43291; MUID:95124710; PMID:7824267
 A:Accession: S43291
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-220 <RES>
 A:Cross-references: GB:S76459; NID:9913479; PIDN:AA33069.1; PID:9913480

Query Match 71.9%; Score 879; DB 2; Length 220;
 Best Local Similarity 82.3%; Pred. No. 1, 1e-70;
 Matches 177; Conservative 5; Mismatches 21; Indels 12; Gaps 3;
 QY 1 MTVLAPAMSPNSLLLLLSPLCRGTGTCYFSSHPISNFKVKFRELTHLXDPVT 60
 Db 1 MTVLAPAMSPNSLLLLLSPLCRGTGTCYFSSHPISNFKVKFRELTHLXDPVT 60

Db 1 MTVLAPAMSPNSLLLLLSPLCRGTGTCYFSSHPISNFKVKFRELTHLXDPVT 60
 QY 61 VAVNLODEKHKALMSLFLAORMIEOLKTVAGSKMOTLLEEDVTEIHFTVSCFQPLPEC 120
 Db 61 VAVNLODEKHKALMSLFLAORMIEOLKTVAGSKMOTLLEEDVTEIHFTVSCFQPLPEC 120
 QY 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNSRCLEVOCCPDSSTLLPPRSPLAEAT 180
 Db 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNSRCLEVOCCPDSSTLLPPRSPLAEAT 180
 QY 177 LEATLEPPRRROLULL-----LLPLTLVLLAA 206
 Db 178 LTAATALLVCQGLLPLVGTSHMFFLPYFLSPSS 212

RESULT 4

FLIT3 ligand - human
 S43291
 C:Species: Homo sapiens (man)
 C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
 C:Accession: S43291
 R:Hanum, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Stocking, S.
 Blood 83, 2795-2801, 1994
 A:Title: Cloning of the human homologue of the murine FLIT3 ligand: a growth factor fo
 A:Reference number: S43290; MUID:94235842; PMID:8190375
 A:Accession: S43291
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-235 <RES>
 A:Cross-references: EMBL:U03858; NID:9494978; PIDN:AA19825.1; PID:9494979
 R:Hanum, S.D.; Stocking, K.; Davidson, H.; Fletcher, F.; Johnson, L.; Escobar, S.
 Oncogene 11, 1165-1172, 1995
 A:Title: Structural analysis of human and murine FLIT3 ligand genomic loci.
 A:Reference number: S43290; MUID:96032581; PMID:7566577
 A:Accession: S43291
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-235 <RES>
 A:Cross-references: EMBL:U029874; NID:91072036; PIDN:AA90949.1; PID:91072037
 R:Hanum, S.D.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;
 felt, A.; Muench, M.; Kelnier, G.; Nankawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
 Nature 368, 643-648, 1994
 A:Title: Ligand for FLIT3/PLK2 receptor tyrosine kinase regulates growth of haematopoietic
 A:Reference number: S43290; MUID:94195428; PMID:8145851
 A:Accession: S43292
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-71, 73-235 <HMAN>
 A:Cross-references: GB:U04806; NID:9483844; PIDN:AA17999.1; PID:9483845
 A:Note: the authors translated the codon AGT for residue 25 as Met
 C:Genetics: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3

Query Match 62.8%; Score 768.5; DB 2; Length 235;
 Best Local Similarity 70.3%; Pred. No. 7, 8e-61;
 Matches 153; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MTVLAPAMSPNSLLLLLSPLCRGTGTCYFSSHPISNFKVKFRELTHLXDPVT 60
 Db 1 MTVLAPAMSPNSLLLLLSPLCRGTGTCYFSSHPISNFKVKFRELTHLXDPVT 60
 QY 61 VAVNLODEKHKALMSLFLAORMIEOLKTVAGSKMOTLLEEDVTEIHFTVSCFQPLPEC 120
 Db 61 VAVNLODEKHKALMSLFLAORMIEOLKTVAGSKMOTLLEEDVTEIHFTVSCFQPLPEC 120
 QY 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNSRCLEVOCCPDSSTLLPPRSPLAEAT 180
 Db 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNSRCLEVOCCPDSSTLLPPRSPLAEAT 180
 QY 177 LEATLEPPRRROLULL-----LLPLTLVLLAA 206
 Db 178 LTAATALLVCQGLLPLVGTSHMFFLPYFLSPSS 212


```

RA Matvei M.G., Rosnet O., Birbaum D., Hannum C.;
RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
CC -! FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
CC FACTORS AND INTERLEUKINS.
CC -! SUBUNIT: Homodimer (soluble isoform) (By similarity).
CC -! SUBCELLULAR LOCATION: Type I membrane protein. Two soluble
CC isoforms are also produced by alternative splicing. One of which,
CC isoform 3/E6, is biologically active, while the other, isoform
CC 4/E6delta16, is inactive.
CC -! ALTERNATIVE PRODUCTS:
CC Event: Alternative splicing; Named isoforms=4:
CC Name=1: Synonyms=6C;
CC IsoId=P49772-1; Sequence=D1Splayed;
CC Name=2: Synonyms=5H;
CC IsoId=P49772-2; Sequence=VSP_004253;
CC Name=3: Synonyms=E6;
CC IsoId=P49772-3; Sequence=VSP_004254, VSP_004255;
CC Name=4: Synonyms=E6delta16;
CC IsoId=P49772-4; Sequence=VSP_004256;
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation at
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (see http://www.isb.ch/announce/isb-ch).
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U04807; AAA18000.1; -
DR EMBL: L23636; AAA39436.1; -
DR EMBL: U29875; AAA90951.1; -
DR EMBL: U29875; AAA90952.1; -
DR EMBL: S76459; AAB33069.1; -
DR EMBL: S76461; AAB33070.1; -
DR EMBL: S76464; AAB33071.1; -
DR EMBL: U04024; AAA93307.1; -
DR EMBL: U04024; AAA93308.1; -
DR PIR: A49265; A49265.
DR MGD: MG1:95560; Flt3l.
DR Interpro: IPR004213; Flt3_Llg.
DR Pfam: PF02947; flt3_lig.1.
KW Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal.
FT SIGNAL 1 26
FT CHAIN 27 232
FT DOMAIN 27 189 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 190 210 POTENTIAL.
FT DOMAIN 211 232 CYTOPLASMIC (POTENTIAL).
FT DISULFID 31 112 BY SIMILARITY.
FT DISULFID 71 156 BY SIMILARITY.
FT DISULFID 120 161 BY SIMILARITY.
FT CARBOHYD 127 127 N-LINKED (GLCNAG...) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAG...) (POTENTIAL).
FT CARBOHYD 232 232 DSITLPKPSIALATELPFRPRQQLLLILL...FLTVLV.
FT VARSPLIC 164 LAAMGIWMORARRRGELHPGVLPDSHP -> GNGGPAAOH
FT FT GAATLTATLALTLVPGCLLPVGSVSHMEFLTPYFIISFS
FT FT LKMVLV (in isoform 2).
FT FT /FTid-VSP_004253.
FT FT DSSTLL->GSHVNG (in isoform 3).
FT FT /FTid-VSP_004254.
FT FT Missing (in isoform 3).
FT FT /FTid-VSP_004255.
FT FT VOCOP -> GLIMQARLTLSNRSOSCLSIVLSGIT (in
FT FT isoform 4).
FT FT /FTid-VSP_004256.
FT FT A->-G (IN REF. 1).
FT FT MISSING (IN REF. 2).
FT FT /FTid-VSP_004257.
FT FT VQCP -> GLIMQARLTLSNRSOSCLSIVLSGIT (in
FT FT isoform 4).
SO CONFLICT 141 141 A->-G (IN REF. 1).
FT SEQUENCE 198 198 MISSING (IN REF. 2).
Query Match 232 AA; 26141 MW; 3A3680D3CH659BA6 CRC64:
Best Local Similarity 99.1%; Score 1212.5; DB : Length 232;
Matches 231: Conservative 0; Mismatches 0; Indels 1; Gaps 2

```

[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2003, 15:45:12 ; Search time 61.4678 Seconds
(without alignments)
969.778 Million cell updates/sec

Title: US-09-448-378-2
Perfect score: 1223
Sequence: 1 MVLAPAWSPNSLLLLLL.....MORARRGELHPGVP1PSHP 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 879 | 71.9 | 172 | 11 | 061104 mus musculu |
| 2 | 842.5 | 68.9 | 169 | 11 | 08VCH4 mus musculu |
| 3 | 779.5 | 63.7 | 292 | 6 | 09GKE0 bos taurus |
| 4 | 774.5 | 63.3 | 292 | 6 | 08MNM1 bos taurus |
| 5 | 774 | 63.3 | 294 | 6 | 09MZV0 bos taurus |
| 6 | 761 | 62.2 | 291 | 6 | 09MKZ9 felis silve |
| 7 | 678.5 | 55.5 | 274 | 6 | 09GKD9 bos taurus |
| 8 | 97.5 | 8.0 | 309 | 10 | 08LKD9 arabidopsi |
| 9 | 96.5 | 7.9 | 318 | 11 | 08CFN3 mus musculu |
| 10 | 95.5 | 7.8 | 909 | 10 | 08L5B3 arabidopsi |
| 11 | 95.5 | 7.8 | 909 | 10 | 08L101 arabidopsi |
| 12 | 95.5 | 7.8 | 909 | 10 | 042484 arabidopsi |
| 13 | 94 | 7.7 | 335 | 4 | 09H665 homo sapien |
| 14 | 93.5 | 7.6 | 510 | 6 | 09B5Y6 macaca fasc |
| 15 | 93.5 | 7.6 | 909 | 10 | 08L3R0 arabidopsi |
| 16 | 93.5 | 7.6 | 909 | 10 | 08L4Y0 arabidopsi |

| | | | | | |
|----|------|-----|------|----|-------------------------------|
| 17 | 93.5 | 7.6 | 909 | 10 | 08L100 arabidopsi |
| 18 | 93.5 | 7.6 | 909 | 10 | 08L4X9 arabidopsi |
| 19 | 93.5 | 7.6 | 909 | 10 | 08L587 arabidopsi |
| 20 | 90.5 | 7.4 | 909 | 10 | 08L3M3 arabidopsi |
| 21 | 90.5 | 7.4 | 909 | 10 | 09ASP5 arabidopsi |
| 22 | 89 | 7.3 | 340 | 6 | 08H290 saginus oe |
| 23 | 89 | 7.3 | 864 | 11 | 08C720 mus musculu |
| 24 | 88.5 | 7.2 | 326 | 12 | 083443 murine rota |
| 25 | 88.5 | 7.2 | 326 | 12 | 083448 murine rota |
| 26 | 88.5 | 7.2 | 493 | 11 | 08BR09 mus musculu |
| 27 | 88.5 | 7.2 | 513 | 11 | 08JZU3 mus musculu |
| 28 | 88.5 | 7.2 | 905 | 10 | 08LXZ8 arabidopsi |
| 29 | 88 | 7.2 | 258 | 4 | 09H563 homo sapien |
| 30 | 88 | 7.2 | 765 | 4 | 094824 homo sapien |
| 31 | 88 | 7.2 | 843 | 4 | 014584 homo sapien |
| 32 | 88 | 7.2 | 1028 | 5 | 08SXA6 Oryzias latipes |
| 33 | 88 | 7.2 | 1254 | 5 | 09VFS1 Oryzias latipes |
| 34 | 87.5 | 7.2 | 477 | 11 | 09CYB2 mus musculu |
| 35 | 87.5 | 7.2 | 1231 | 10 | 09FKE2 Arabidopsis thaliana |
| 36 | 87 | 7.1 | 291 | 16 | 09ZB99 Arabidopsis thaliana |
| 37 | 87 | 7.1 | 809 | 11 | 08CAB2 Arabidopsis thaliana |
| 38 | 87 | 7.1 | 1256 | 5 | 09VFS0 Arabidopsis thaliana |
| 39 | 86.5 | 7.1 | 2111 | 5 | 091802 Arabidopsis thaliana |
| 40 | 86.5 | 7.1 | 4167 | 5 | 09GPN8 Arabidopsis thaliana |
| 41 | 86 | 7.0 | 962 | 5 | 096164 Arabidopsis thaliana |
| 42 | 85 | 7.0 | 181 | 5 | 017726 Caenorhabditis elegans |
| 43 | 85 | 7.0 | 1305 | 2 | 006521 Enterococcus faecalis |
| 44 | 85 | 7.0 | 4513 | 10 | 09MBF8 Arabidopsis thaliana |
| 45 | 84.5 | 6.9 | 364 | 4 | 096AY5 Homo sapien |

ALIGNMENTS

| | | | | |
|-----------------------|---|--------------------|-----------|-------------|
| RESULT 1 | 651104 | PRELIMINARY: | PRT: | 172 AA. |
| AC | 061104: | | | |
| DI | 01-NOV-1996 (TREMBLrel. 01, Created) | | | |
| DI | 01-NOV-1996 (TREMBLrel. 01, Last sequence update) | | | |
| DI | 01-NOV-2003 (TREMBLrel. 23, Last annotation update) | | | |
| DE | Flt3 ligand, T169 form. | | | |
| CN | Flt3L. | | | |
| OS | Mus musculus (Mouse) | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| CX | NCBI_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| EA | McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Jacobs K., | | | |
| EA | Mattison J., Tsai S., Luh J., Guimaraes M., Mattei M.-G., Rosnet C., | | | |
| FA | Birbaumer D., Hahnemann C., | | | |
| RT | "Flt3 ligand" expression, genomic organization, alternatively spliced | | | |
| RT | forms and processing." | | | |
| RL | Submitted (DEC-1995) to the EMBL/Genbank/DBJ databases. | | | |
| DR | EMBL: U44024; AA93305.1; - | | | |
| DR | HSSP: P49771; IETF. | | | |
| DR | MCD: MG1:95560; F1C31. | | | |
| DR | InterPro: IPR004213; Flt3_lig. | | | |
| DR | Pfam: PF02947; flt3_lig. 1. | | | |
| SO | SEQUENCE 172 AA; 19465 MW; 04FOA01071E3384 CRC64; | | | |
| Query Match | 71.9% | Score 879; | DB 11; | Length 172; |
| Best Local Similarity | 98.2% | Pred. No. 1.2e-81; | | |
| Matches 165; | Conservative 1; | Mismatches 2; | Indels 0; | Gaps 0; |
| QY | 1 MVLAPAWSPNSLLLLLLSPCLRGFPDYSFSSPISNFKVFRRLTHLNDYVT 60 | | | |
| DB | 1 MVLAPAWSPNSLLLLLLSPCLRGFPDYSFSSPISNFKVFRRLTHLNDYVT 60 | | | |
| QY | 61 VAVNIODEKHCXALSLFIAQWIEQLTVAGSKMGLLEVDNTEIHVFSTCTOPLDEC 120 | | | |
| DB | 61 VAVNIODEKHCXALSLFIAQWIEQLTVAGSKMGLLEVDNTEIHVFSTCTOPLDEC 120 | | | |

OY 121 LRFVOTNISHLLKDTCTOLALKPCIGKACONFSKCLEVOCQPSSTL 168
 Db 121 LRFVOTNISHLLKDTCTOLALKPCIGKACONFSKCLEVOCQPSSTL 168

RESULT 2

O8VCH4 PRELIMINARY: PRT: 169 AA.

DT 01-MAR-2002 (TREMblrel. 20, Created)

DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)

DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)

DE Similar to FMS-like tyrosine kinase 3 ligand.

GN FLT3L.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

PC TISSUE=Liver;

RA Strausberg R.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC019801; AAH19801.1; -

DR MGD: MGI:95560; FLT3L

DR InterPro: IPR004213; FLT3_Lig.

DR Pfam: PF02947; FLT3_Lig. 1.

KW Kinase.

SQ SEQUENCE 169 AA: 18986 MW: 58464709724EPFZ CRC64:

Query Match 68.9%; Score 842.5; DB 11: Length 169;

Best Local Similarity 92.5%; Pred. No. 6e-78;

Matches 161; Conservative 0; Mismatches 4; Indels 9; Gaps 1;

OY 1 MTVLAPAMSPNSLLILLLISPCLRGPDGCFYSHSPSSNFKYKFEITDHLKDYPT 63

Db 1 MTVLAPAMSPNSLLILLLISPCLRGPDGCFYSHSPSSNFKYKFEITDHLKDYPT 63

OY 61 VAVNIODEKHCKALMSLFLAORWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFQPLPFC 120

Db 61 VAVNIODEKHCKALMSLFLAORWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFQPLPFC 120

OY 121 LRFVOTNISHLLKDTCTOLALKPCIGKACONFSKCLEVOCQPSSTLPPRSP 174

Db 121 LRFVOTNISHLLKDTCTOLALKPCIGKACONFSKCLEVOCQPSSTLPPRSP 165

RESULT 3

O9GKEO PRELIMINARY: PRT: 292 AA.

DT 01-MAR-2001 (TREMblrel. 16, Created)

DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)

DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)

DE FLT3 ligand isoform-1.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-20570936; PubMed-11120823;

RA Mwangi W., Brown W.C., Palmer G.H.;

RT "Identification of fetal liver tyrosine kinase 3 (FLT3) ligand domain

RT required for receptor binding and function using naturally occurring

KT ligand isoforms."

RL J. Immunol. 165:6966-6974(2000).

DR EMBL: AF282985; AAF93322.1; -

DR HSSP: P49771; IETE.

DR InterPro: IPR004213; FLT3_Lig.

DR Pfam: PF02947; FLT3_Lig. 1.

SQ SEQUENCE 292 AA: 32390 MW: D68B9ED79221202D CRC64:

Query Match 63.7%; Score 779.5; DB 6: Length 292;

Best Local Similarity 63.2%; Pred. No. 3e-71;

Matches 165; Conservative 20; Mismatches 43; Indels 33; Gaps 5;

OY 1 MTVLAPAMSPNSLLILLLISPCLRGPDGCFYSHSPSSNFKYKFEITDHLKDYPT 60

Db 1 MTVLAPAMSPNSLLILLLISPCLRGPDGCFYSHSPSSNFKYKFEITDHLKDYPT 60

OY 61 VAVNIODEKHCKALMSLFLAORWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFQPLPFC 120

Db 61 VAVNIODEKHCKALMSLFLAORWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFQPLPFC 120

OY 121 LRFVOTNISHLLKDTCTOLALKPCIGKACONFSKCLEVOCQPSSTLPPRSPALPAT 180

Db 121 LRFVOTNISHLLKDTCTOLALKPCIGKACONFSKCLEVOCQPSSTLPPRSPALPAT 178

OY 181 ELPEPR-PROQLDILLLPLTLVLAAMGL-RMGRARRR----- 218

Db 179 SLPGQSPPLLLILLILLLPLVALLLATAWGLRMGRARRRTRYPGERRRRLRPRESSHLPA 238

OY 219 -----GELHPGVPLPSHP 231

Db 239 DIESELKGSOLRPG-PTLGH 258

RESULT 4

O8NMW1 PRELIMINARY: PRT: 292 AA.

DT 01-MAR-2002 (TREMblrel. 20, Created)

DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)

DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)

DE FLT3 ligand.

GN FLT3 ligand.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RA Hirono H., Momotani E.;

RT "Cloning of a cDNA for bovine FLT3 ligand."

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB05-841; BAB79634.1; -

DR InterPro: IPR004213; FLT3_Lig.

DR Pfam: PF02947; FLT3_Lig. 1.

SQ SEQUENCE 292 AA: 32388 MW: 2A797E0C1199C1D9 CRC64:

Query Match 63.3%; Score 774.5; DB 6: Length 292;

Best Local Similarity 62.8%; Pred. No. 9.6e-71;

Matches 164; Conservative 20; Mismatches 44; Indels 33; Gaps 5;

OY 1 MTVLAPAMSPNSLLILLLISPCLRGPDGCFYSHSPSSNFKYKFEITDHLKDYPT 60

Db 1 MTVLAPAMSPNSLLILLLISPCLRGPDGCFYSHSPSSNFKYKFEITDHLKDYPT 60

OY 61 VAVNIODEKHCKALMSLFLAORWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFQPLPFC 120

Db 61 VAVNIODEKHCKALMSLFLAORWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFQPLPFC 120

OY 121 LRFVOTNISHLLKDTCTOLALKPCIGKACONFSKCLEVOCQPSSTLPPRSPALPAT 180

Db 121 LRFVOTNISHLLKDTCTOLALKPCIGKACONFSKCLEVOCQPSSTLPPRSPALPAT 178

OY 181 ELPEPR-PROQLDILLLPLTLVLAAMGL-RMGRARRR----- 218

Db 179 SLPGQSPPLLLILLILLLPLVALLLATAWGLRMGRARRRTRYPGERRRRLRPRESSHLPA 238

OY 219 -----GELHPGVPLPSHP 231

Db 239 DIESELKGSOLRPG-PTLGH 258